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Winkler, Ulrike Thursday, November 21, 2002 3:20 PM STIC-Biotech/ChemLib

STIC,

Please search SEQ ID 48 and 51 of application 09/670105 please limit the search results to oligos that are 50 nt or less.

Thanks, Ulrike

Ulrike Winkler, Ph.D. Patent Examiner Crystal Mall 1, 8D09 1911 South Clark Place Arlington, VA 22202 tel. 703-308-8294 fax. 703-308-4426

> Mary Jane Ruhl Tech. Info. Specialist, STIC TC-1600 CM-1, Room 6A-06 Phone: 605-1155

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Searcher:
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TYPE OF SEARCH:
NA Sequences:
AA Sequences:
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Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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BioTech-Chem Library Search Results Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258 CM-1 Room 1E01

Voluntary Results Feedback Form
I am an examiner in Workgroup: (Example: 1610)
Relevant prior art found, search results used as follows:
102 rejection
103 rejection
Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
Foreign Patent(s)
Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Search results were not useful in determining patentability or understanding the invention.
Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or e-mail mary.hale@uspto.gov.

42.3 32 13 B1192552 B1192552 G02945447 42.3 32 17 AZ28809 AZ28209 AZ28209 AZ282139 AZ2823139 AZ282333 AZ283333 AZ28333 AZZ83333 A	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts blasmid inserts. Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 4112, USA Fel: 801 885 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00
C 7 C 9 C 9 C 10 C 11 D 11 C 12 C 12 C 13 D 19	TITLE JOURNAL COMMENT
Compugen Ltd. ; Search time 1611.47 Seconds (without alignments) 261.304 Million cell updates/sec c 26 meters: 102860	1 to the score of the result being printed, of the total score distribution. SUMMARIES Description
Gen Gen Croth usi 5, 200 5, 200 6, 200 CCTGCTGC CO Gap Seqs, 8 Sthu:* Sthu:* Sthu:* Stro:* Sthu:* Sthu:* Sthu:* Sthu:* Sthu:* Sthu:* Sthu:* Sthu:* Sthu:* Sthu:* Stro:*	the number of than or equal by analysis ch Length DB ch Length DB ch 2 30 17 2 42 17 2 46 9 2 3 2 17 3 2 17 3 3 2 17 3 3 2 17 3 3 2 17 3 3 3 0 12
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Luna,D., AoyajiA., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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                                                                                                                                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Length: 10000 Std Error: 0.00
                 Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
Plate: 0317 row: J column: 04
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Fax: 801 585 7177
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/Jab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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(http://www.jax.org/resources/documents/dnares/). The DNA
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10.5 kb range using preparative agancse gel
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampleillin resistance."
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Al581188.1 GI:4565564
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                   /strain="C57BL/6J"
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Plate: 0421 row: D column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Matches 12; Conservative
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Unpublished (1997)
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constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucel (TRED9274 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 30)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602440944F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4556602 5'
                   Gaps
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1 (bases 1 to 29)
Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
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T. brucei sheared genomic DNA clone 36b10, forward sequence, genomic survey sequence.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/strain="TREU927"
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/clone="36b10"
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In project, 1

See Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

Na Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh(@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA 180-lated from a cloned population of
Trypanosoma brucel (TRED927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucel/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                              /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"
                                                                                                                                                                                                                       /clone="IMAGE:2154774"
/clone_lib="NCI_CGAP_CO14"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH108"
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/strain="TREU927"
Trace considered overall poor quality Insert Length: 829 Std Error: 0.00 Seq primer: -40UP from Glbco High quality sequence stop: 1 POLYA-NO.
                                                                                                                                                                           /organism-"Homo sapiens"
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/organism="Homo saptens"
/db_xref="taxon:9606"
/clone="InAGE:455602"
/clone="Inb="NIH_MGC_75"
/clone="Inb="NIH_MGC_75"
/clone="Inb="NIH_MGC_75"
/clone="Inb="NIH_MGC_75"
/lab_host="NIH_MGC_75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGGCCGACATAATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACATAATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACATAATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACATAATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACATAATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGACATAATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGGCCATAATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGGCCATAATGGCCATAATGGCCATAGGCCATAATGGCCATAGGCCATAATGGCCATAATGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGCCATAGGC
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1. (bases 1 to 32)

2. (NIH-MGC http://mgc.nci.nih.gov/.

3. NIH-MGC http://mgc.nci.nih.gov/.

3. NIH-MGC http://mgc.nci.nih.gov/.

4. (Droublished (1999)

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                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
   Tissue Procurement: CLONTECH Laboratories, Inc.
   CDNA Library Preparation: CLONTECH Laboratories, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
   http://mage.lln.gov
   Plate: LLCM1259 row: h column: 11
   High quality sequence stop: 24.
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/db_xref="taxon:9606"
/clone="IMAGE:5088947"
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Matches 11; Conservative
    Unpublished (1999)
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/issue_trpe="epithelioid carcinoma cell line"
/lab_host="Entholioid carcinoma cell line"
/lab_host="DH10B (phage_resistant)"
/note="Organ: pancreas; vector: pdrB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
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1 (bases 1 to 32)

2 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., , Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

IL Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002 DNA linear GSS 27-APR-2001 2M0271N2IR Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0271N2I R, DNA sequence.
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/lab_host="E. coli strain XLIO-Gold, Tl-resistant, F-"
/lab_host="S. explain: Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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/clone="UUGC2M0271N21"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.3%; Score 11; DB 13; Length 32; 100.0%; Pred. No. 5.5e+04; ive 0; Mismatches 0; Indels
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/strain="C57BL/6J"
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High quality sequence stop: 32.
Location/Qualifiers
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Insert Length: 10000 Std Err
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Matches 11; Conservative
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11; Conservative
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Medicago sativa
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwMD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygli; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopeerygli; Percomorpha; Atherinomorpha; Acanthopeerygli; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.

1. (bases 1 to 34)

1. (bases 1 to 34)

1. Medaka EST Project in Takeda's lab

1. Medaka EST Project in Takeda's lab

1. Unpublished (2001)

1. Contact: Tadasu Shin-i

1. Fata Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Fax: 81-559-81-6855
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/dev_stage="segmentation stage 20 - 25"
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/db_xref="taxon:8090"
/clone="MFO1SSA004B08"
/clone_lib="MFO1SSA CDNA"
/sex="mixture of female and male"
                                                                                                                                                                                                                                                                                          42.3%; Score 11; DB 17; L
100.0%; Pred. No. 5.5e+04;
tive 0; Mismatches 0;
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Location/Qualifiers
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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BJ001219
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1. .37
/organism="Homo sapiens"
/do_xref="texton:9606"
/clone_lib="NCI_CGAP_CLLI"
/tissue_type="B-cell, chronic lymphotic leukemia"
/tab_host="B-cell, chronic lymphotic leukemia"
/tab_host="B-cell, chronic lymphotic leukemia"
/lab_host="B-cell, chronic leukemia"
/lab_host="B-cell, chroni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: A.D., Ph.D.,
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Geome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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AI077338 37 bp mRNA linear EST 24-SEP-1998 oy65902.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1670738 3' similar to TR:Q64657 Q64657 INTEGRIN BETA 5 SUBUNIT ;, mRNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
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/organism="Mus musculus"
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Best Local Similarity
Matches 11; Conserv
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                            /organism="Medicago sativa"
//cultivar="Riley X KS224"
//cultivar="Riley X KS224"
//cultivar="taxon:3819"
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//tissue_type="Leaf and stem"
//note="glandular-haired versus non-glandular-haired
/note="glandular-haired versus non-glandular-haired subtraction with CLONTECH PCR-Select cDNA subtraction."
                                                         Expressed sequence tags subtracted in reciprocal fashion between glandular-haired and non-glandular-haired full sibs of alfalfa Unpublished (2000)
Contact: Hays GMPRC, PSERU; Department of Agronomy
Kansas State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vz8304.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:1333110 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHASE,
MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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The WashU-HHMI Mouse EST Project
Unpublished (1994)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
1.40
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                                                                                                                                                                             Throckmorton Hall, Manhattan, KS 66506, USA Tel: 785 532 7116
Rax: 785 532 6167
Email: dhays@genes.alfalfa.ksu.edu
Seq primer: SP6.
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                     1 (bases 1 to 37)
Hays, D. and Skinner, D.
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Best Local Similarity
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/db_xref="taxon:10090"
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/clone_lib="soares_mammary_gland_NbMMG"
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/clone_lib="soares_mammary_gland"
/dev_stage="4 weeks"
/dev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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Marra,M., Hillier,L., Allen,M., Bowles,M., Ditetrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Tel: 314 286 1800
Fax: 314 286 1810
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Possible reversed clone: similarity on wrong strand
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Unpublished (1996)
Contact: Marza MyMouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
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/strain="C57BL"
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/clone="IMAGE:1499113"
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High quality sequence stop: 1.
Location/Qualifiers
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                                                              /note="Vector: pME185-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ArTGGGCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTGTAAAAGCTGGG and 3' end primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ832139 40 bp DNA linear GSS 20-FEB-2001 2M0112P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112P14 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT. 2, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="UGCZM0112P14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/clone_lib="Sugano mouse embryo mewa"
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Insert Length: 10000 Std Error: 0.00
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                     /dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.3
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CIGCIGCICCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 crecrecrec 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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84112,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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AZ832139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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QQ ò

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114 (jplART29072.1), a copyrnumber inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampleillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 bp DNA linear GSS 13-DEC-2000 clone UUGCIMO467D15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic AZ626793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 41)
Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Welss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/strain="c57BL/6J"
/db_xref="taxon:10090"
/dboore="UGCIM0467D15"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.3%; Score 11; DB 17; Length 40; 100.0%; Pred. No. 5.6e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
insert Length: 10000 Std Error: 0.00
Plate: 0467 row: D column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ626793.1 GI:11748983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 TTCCTGCTGCT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 TTCCTGCTGCT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gell electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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13 BASE COUNT ORIGIN

.; 0 0; Gaps Ouery Match 42.3%; Score 11; DB 17; Length 41; Best Local Similarity 100.0%; Pred. No. 5.7e+04; Matches 11; Conservative 0; Mismatches 0; Indels

ŏ QQ

Search completed: December 6, 2002, 00:45:10 Job time : 1613.47 secs

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5, 2002, 20:34:23; Search time 48.8163 Seconds (without alignments) 163.339 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    1 GIGCIICCIGCIGCICCCAAGAACCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                             441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                   OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_NA:*
                                                                                                                                                                                                                                             US-09-670-105-51
26
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                                                                                                                                                     December
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                                                                                                                                                                                                                                                Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                  Run on:
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APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
ATTORNEY AGENT INFORMATION:
NAME: MSYSTEM INFORMATION:
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0062-02000
TELEPHONE: (202)408-4000
TELEPHONE: (202)408-4400
INFORMATION FOR SEQ 1D NO: 51:
SEQUENCE CHARACTERISTICS:

PRIOR APPLICATION DATA:

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                                                                                                                                                                                                                                                  Sequence 6, Application US/08442010
Patent No. 584994
GENERAL INFORMATION:
APPLICANT: NARAYAN, Opendra
TITLE OF INVENTION: Animal Model for HIV-1 Induced Disease
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: ADDRESSE: BANNER & WITCOFF, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
    Ouery Match 100.0%; Score 26; DB 4; Length 26; Best Local Similarity 100.0%; Pred. No. 5.1e-05; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Library Compalatory
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,010
FILING DATE: 16-MAY 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: CHAO, MAIK
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,645
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEPHONE: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..27
OTHER INFORMATION: /note= "complementary to HXBc2
OTHER INFORMATION: (gpl20) 7810-7784"
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Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 26; Conservative 0; Mismatches 0;
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                                                                                              1 GTGCTTCCTGCTGCTCCCAAGAACCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: SIGGE
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PCR primer
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GIGCIICCIGCICCCCAAGAACCC 26
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APPLICANT: Zhang, Lingi
APPLICANT: Lewin, Sharon R
APPLICANT: Kostrikis, Leondios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STATE: Illinois
COUNTRY: USA
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US-08-442-010-6
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    Query Match
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Sequence 52, Application US/09092077

Fatent No. 6194142

GENERAL INFORMATION:
APPLICANT: Moncany, Maurice
APPLICANT: Montagnier, Luc
TITLE OF INVENTION: Nuclectide Sequences Derived From The
TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
TITLE OF INVENTION: Genomes Of These Retroviruses And For The Amplification Of The
TITLE OF INVENTION: Of The Diseases Due To Those Viruses
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             ö
                                                                                                                                                                                                             Gaps
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                                                                                                                                                         'Match 100.0%; Score 26; DB 4; Length 26; Local Similarity 100.0%; Pred. No. 5.1e-05; les 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

. IP: 20005-3315

. COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE-YOCKET NUMBER: 02356.0062-02000
TELECOMMUNICATION INFORMATION:
TELECHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/472,928
FILING DATE: 07-JUN-1995
APPLICATION UNMBER: US 08/160,465
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              APPLICATION NUMBER: FR 8912371
FILING DATE: 20-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                    HOLECULE TYPE: DNA (genomic) US-09-092-077-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 base pairs
                       TYPE: nucleic acid
STRANDEDNESS: single
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EDNESS: single
                                                                    linear
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US-09-092-077-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                         Query Match
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
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Query Match
Best Local Similarity
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                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-471-770-34
                                                                                                                                                COUNTRY:
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TITLE OF INVENTION: METHOD FOR IDENTIFYING GENOMIC EQUIVALENT MARKERS AND TITLE OF INVENTION: THERE USE IN QUANTITATING CELLS AND POLYNUCLEOTIDE TITLE OF INVENTION: SEQUENCES THEREIN STATE OF INVENTIONS SEQUENCES THEREIN CURRENT APPLICATION NUMBER: US/09/481,288 CURRENT PILING DATE: 2000-01-11 NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 23 LENGTH: 24
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US-08-679-493A-32/C
US-08-679-493A-32/C
Squence 32, Application US/08679493A
Patent No. 6303295
GENERAL INFORMATION:
APPLICANT: Taylor, Ethan W.
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT APPLICATION NUMBER: 06/001203
PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-01-14
PRIOR FILING DATE: 1995-00-16
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 32
LENGTH: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/08470202
Patent No. 5759808
GENERAL INFORMATION:
APPLICANT: Guertier, Lutz G.
APPLICANT: Brunn, Albrecht v.
APPLICANT: Brunn, Albrecht v.
APPLICANT: Rauge, Stefan
APPLICANT: Rauser, Hans-Peter
TITLE OF INVENTION: Retrovirus from the HIV Group and Its
TITLE OF INVENTION: 058
NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.8%; Score 21; DB 4; Length 38; 100.0%; Pred. No. 0.018; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.5%; Score 23; DB 4; Best Local Similarity 100.0%; Pred. No. 0.0017; Matches 23; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: RNA
; ORGANISM: Human immunodeficiency virus type 1
US-08-679-493A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GIGCTICCTGCTGCTCCCAAGAA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.C
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
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Gaps
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APPLICANT: Guertler, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht v.
APPLICANT: Anapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Retrovirus from the HIV Group and Its
TITLE OF SEQUENCES: 63
CORRESPONDENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.9%; Score 20; DB 1; Length 24; 100.0%; Pred. No. 0.057; tive 0; Mismatches 0; Indels
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ADDRESSEE: Dunner
                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05495-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                   APPLICATION: 435
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-0CT-1993
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-0CT-1992
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
APPLICATION NUMBER: DE P 42 35 718.7
TITING DATE: 22-0CT-1992
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                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 01-UN-1993
ATTONENY, AGGENT INFORMATION:
NAME: MICHAEL J. Blake
REGISTRATION NUMBER: 37,096
                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08471770 Patent No. 5770427
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STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 24 base pairs
TYPE: nucleic acid
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Gaps
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Sequence 34, Application US/09109916

Patent No. 6277561

GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
APPLICANT: Brunn, Albrecht V.
APPLICANT: Brunn, Albrecht V.
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVINUS FROM HIV GROUP AND ITS USE
FILE REPERENCE: 05495.0001-04

CURRENT APPLICATION NUMBER: US/09/109,916

CURRENT FILING DATE: 1998-07-02

EARLIER APPLICATION NUMBER: DE P 42 33 646.5

EARLIER FILING DATE: 1992-10-06

EARLIER FILING DATE: 1992-10-06

EARLIER FILING DATE: 1992-12-30

EARLIER FILING DATE: 1992-12-30

SARLIER PELING DATE: 1993-10-06

SARLIER RELING DATE: 1993-06-01

NUMBER OF SGO ID NOS: 67

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.9%; Score 20; DB 2; Length 24; Best Local Similarity 100.0%; Pred. No. 0.057; Matches 20; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUBTRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,653
FILING DATE: 05-CUT-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-CCT-1992
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-CCT-1992
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 30-DEC-1992
PRIOR APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: CAICAI P. EILBAUGI
RECISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 05495-0001-02000
TELEPHONE: 202-408-4400
TELEPHONE: 202-408-4400
TELEPHONE: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) US-08-468-059-34
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 1; Length 24;
Pred. No. 0.057;
0; Mismatches 0; Indels
                   COMPUTER READBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/471,770
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DAFE: 05-0CT-1993
FILING DAFE: 05-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 22-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-0CT-1992
FILING DATE: 30-DEC-1992
FILING DATE: 30-DEC-1992
FILING DATE: 30-DEC-1993
ATTORNEY-AGENT INFORMATION:
NAME: CATOL P: BIDAUGH
REGISTRATION NUMBER: DE P 43 18 186.4
FILING DATE: 01-JUN-1993
ATTORNEY-AGENT INFORMATION:
NAME: CATOL P: BIDAUGH
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 05495-0001-03000
TELECOMMUNICATION INFORMATION:
NAME: CATOL P: BIDAUGH
REFERENCE/DOCKET NUMBER: 05495-0001-03000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/08468059
Patent No. 5840480
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
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Best Local Similarity 100.
Matches 20; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                    STATE: CA
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US-08-472-756-2
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                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: SHERIDAN, PATRICK J.

APPLICANT: GAGNE, JULIO C.

APPLICANT: GAGNE, JULIO C.

APPLICANT: LUDTKE, DOUGLAS N.

APPLICANT: LUDTKE, DOUGLAS N.

TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY

TITLE OF INVENTION: ENZYME INHIBITION ASSAY

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: primer US-09-109-916-34
                                                                                                                                                               Query Match 76.9%; Score 20; DB 4; Length 24; Best Local Similarity 100.0%; Pred. No. 0.057; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 05/08/472,756

FILING DATE: 07/095

CLASSIFICATION: 435

ATTONREY/AGENT INPORMATION:

NAME: GOLDMAN ESQ., 84,174

REGISTRATION NUMBER: 34,174

REGISTRATION NUMBER: 34,174

REGISTRATION NUMBER: 1014.001

TELEPHONE: (510) 601-2719

TELEPHONE: (510) 601-2719

TELEPHONE: (510) 655-3542

INPORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.1%; Score 19; DB 100.0%; Pred. No. 0.11:1ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CALIFORNIA
COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-610-955-5
; Sequence 5, Application US/08610955
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08472756 Patent No. 5780227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
SEQ ID NO 34
LEWTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                             7 CCTGCTGCTCCCAAGAACCC 26
                                                                                                                                                                                                                                                                                     1 CCTGCTCCCAAGAACCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TICCTGCTCCTCCAAGAA 23
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94608
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                                                                                                                                                                                                                                                                                                                                                                      US-08-472-756-5
                                                                                  FEATURE:
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GENERAL INFORMATION:
APPLICANT: SHERIDAN, PATRICK J.
APPLICANT: GAGNE, JULIO C.
APPLICANT: GAGNE, JULIO C.
APPLICANT: LUDTKE, DOUGLAS N.
TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
TITLE OF INVENTION: ENZYME INHIBITION ASSAY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                       APPLICANT: ANDERSON, MARY L.
APPLICANT: LUDTKE, DOUGLAS N.
TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
TITLE OF INVENTION: ENZYME INHIBITION ASSAY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORRON STREET
CITYLE OF THE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.1%; Score 19; DB 2; Length 36; 100.0%; Pred. No. 0.18; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/610,955
FILING DATE: 05-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,756
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN ESO., KENNETH M.
REGISTRATION NUMBER: 34,174
REGISTRATION NUMBER: 34,174
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 1014.001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      COUNTRY: UNITED STATES
ZIP: 94608
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08472756 Patent No. 5780227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHIRON CORPORATION
APPLICANT: SHERIDAN, PATRICK J. APPLICANT: GAGNE, JULIO C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CALIFORNIA
COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TICCIGCIGCICCCAAGAA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                     CALIFORNIA
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Matches 19; Conserv
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Gaps
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Use
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GENERAL INCRMATION:
APPLICANT: Guertler, Lutz G.
APPLICANT: Brunn, Albrecht v.
APPLICANT: Raupp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Retrovirus from the HIV Group and It
TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                   Query Match 69.2%; Score 18; DB 2; Length 18; Best Local Similarity 100.0%; Pred. No. 0.59; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05495-0001-00000
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PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-0CT-1993
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-0CT-1992
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-0CT-1992
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFICE PATENTING RELEASE #1
                                                                                                                                                                                                                                                                                                                                                                                      US-08-470-202-27
; Sequence 27, Application US/08470202
; Patent No. 5759808
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-610-955-2
                                                                                                                                                                                                                                                                              1 TCCTGCTGCTCCCAAGAA 18
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REGISTRATION NUMBER: 37
                                                                                                                                                                                                                                                    6 TCCTGCTGCTCCCAAGAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-400
THETEPHONE: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 base pairs
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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STRANDEDNESS: single
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Patent No. 5853974
GENERAL INFORMATION:
APPLICANT: SHERIDAN, PATRICK J.
APPLICANT: GAGNE, JULIO C.
APPLICANT: LUDTKE, DOUGLAS N.
TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
TITLE OF INVENTION: ENZYME INHIBITION ASSAY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DA PC COMPATIBLE
COMPUTER: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/610,955
FILING DATE: 05-MAR-1996
CLASSIFICATION: 435
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/472,756
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                      ATTORNEY AGENT INFO WATTON:
NAME: GOLDMAN ESO., KENNETH M.
REGISTRATION NUMBER: 34.174
REFERENCE/DOCKET NUMBER: 1014.001
TELECOMMUNICATION INFORMATION:
TELEFAN: (510) 601-2719
TELEFAN: (510) 601-2719
TELEFAN: (510) 6055-3542
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: GOLDMAN ESQ., KENNETH M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 1014.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2119
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,756
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 4560 HORTON STREET CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 TCCTGCTGCTCCCAAGAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCCTGCTGCTCCCAAGAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CALTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-08-610-955-2
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Search completed: December 5, 2002, 22:51:15 Job time: 49.8163 secs
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APPLICANT: Guertler, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht v.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Retrovirus from the HIV Group and Its
TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                       Length 40;
                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAITIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,770
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 20-OCT-1992
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION NUMBER: DE P 42 18 186.4
FILING DATE: 01-JUN-1993
APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: CATOL P. ELIABAGI.
REGISTRATION NUMBER: 32,220
                                                                  Ouery Match 69.2%; Score 18; DB 1; Best Local Similarity 100.0%; Pred. No. 0.58; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32,220
FFR: 05495-0001-03000
                                                                                                                                                                                                                                                                                  RESULT 15
US-08-471-770-27
; Sequence 27, Application US/08471770
; Patent No. 5770427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOCOGY: linear;
; MOLECULE TYPE: DNA (genomic)
US-08-471-770-27
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
; MOLECULE TYPE: DNA (genomic) US-08-470-202-27
                                                                                                                                                                                          19 TGCTGCTCCCAAGAACCC 36
                                                                                                                                                                 9 TGCTGCTCCCAAGAACCC 26
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TYPE: nucleic acid
STRANDEDNESS: single
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                                Gaps
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69.2%; Score 18; DB 1; Length 40; 100.0%; Pred. No. 0.58; 1ive 0; Mismatches 0; Indels
                                                           9 TGCTGCTCCCAAGAACCC 26
                                                                            19 TGCTGCTCCCAAGAACCC 36
Query Match 69.2%
Best Local Similarity 100.(
Matches 18; Conservative
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Pseudoknot oligonu env d primer. Syn HIV-2 PCR primer e Label extender bla

PCR primer for Hlv RRE oligonucleotid

Primer ED12

HIV Rev response e 3v3longdegi primer Capture extender P

HIV-1 PCR primer 3
Human immunodefici
PCR primer GP40F1.
HIV-1 9p120 DNA pr
Sequence of primer
PCR primer used in
HIV primer 1. Syn
sk68 primer. Syn
PCR primer SK 68
Primer S

Scoring table:

Word size :

Jatabase

Searched:

Perfect score:

Sequence:

OM nucleic

Run on:

Peptide nucleic ac Human immunodefici HERV-W envelope pr Human CETP hairpin

HIV-1 PCR primer s Ineffective anti-H Oligonuclectide #1

Dog genomic marker Enzymatic RNA mole Human WT1 truncati

Dombrock (a) antig Dombrock (b) antig

New nucleotide sequences derived from genome of HIV-1, HIV-2 and SIV - useful as primers for amplification of immuno-deficiency viruses in diagnosis and for raising antibodies in treatment of HIV infections

Moncany M, Montagnier L;

WPI; 1990-378039/51.

MMY8bis nucleotide
Human or simian im
Human or simian im
PCR primer for SIV
Human immunodefici

AAQ06939 AAT98046 AAT98047 AAV08911 AAQ81321 AAT35934 AAX25184

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Score

Result Š. HIV env PCR primer HIV-1 group O gp41 HIV-1 env gene amp

Dombrock carrier m

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MMy8 nucleotide constituent of env gene of HIV-1 Bru, HIV-1 Mal and HIV-1 \rm Eli.
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                                                   AAT74060
AAT74050
AAT74057
AAC58951
AAX22352
ABK65874
AAX6123
AAA76123
AAA00536
AAQ38852
AAQ38852
AAQ38959
                                                                                                                                                                                                                                     AAQ98006
ABK65879
AAH20074
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ABK69683
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                                                                                                                                                                                                                             AAQ14985
                                                                                                                                                                                                                                                                                 AAA66386
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(INRM ) INSERM INST NAT SANTE
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04045088580410444557777747747474747
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05-JUN-1990;
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AAQ06938;
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                                                                     (without alignments)
251.936 Million cell updates/sec
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2. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
8: /SIDS2/gcgdata/geneseq-embl/NA1980.DAT:*
11: /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1980.DAT:*
12: /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:*
14: /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:*
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18: /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:*
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19: /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:*
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22: /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:*
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                                                             2002, 21:44:53 ; Search time 232.408 Seconds
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        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                               2185239 seqs, 1125999159 residues
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                                                                                                                  1 GTGCTTCCTGCTGCTCCCAAGAACCC
                                           - nucleic search, using sw model
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Match
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AAT98046 standard; DNA; 26
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AAT98047/c
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AAT98046
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                          This nucleotide sequence is found in posn. 7857-7832 of HIV-1 Bru, 7846-7821 of HIV-1 Mal and 7800-7775 of HIV-1 Eli. It is the antisense strand of a primer pair used to amplify these HIV-1 viral sequences, esp. in conjunction with in vitro diagnosis of infection. It is useful for treating viral diseases, eg. AIDS.
See also AAQ06905-37 and AAQ06939-54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This nucleotide sequence is found in posn. 7832-7857 of HIV-1 Bru, 7821-7846 of HIV-1 Mal and 7755-7800 of HIV-1 Eli. It is the sense strand of a primer pair used to amplify these HIV-1 viral sequences, esp. in conjunction with in vitro diagnosis of infection. This sequence can be expressed in host cells to produce a translation prod. useful, in an immunogen, along with Abs raised against it.
                                                                                                                                                                                                                                                                                                       ΜΜγθbis nucleotide constituent of env gene of HIV-1 Bru, HIV-1 Mal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleotide sequences derived from genome of HIV-1, HIV-2 and SIV - useful as primers for amplification of immuno-deficiency viruses in diagnosis and for raising antibodies in treatment of HIV infections
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100.0%; Pred. No. 0.00026;
ive 0; Mismatches 0;
                                                                                                                        100.0%; Score 26; DB 11;
100.0%; Pred. No. 0.00026;
iive 0; Mismatches 0;
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                                                                                                     Sequence 26 BP; 4 A; 11 C; 5 G; 6 T; 0 other;
                                                                                                                                                                              1 GTGCTTCCTGCTGCTCCCAAGAACCC 26
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(INRM ) INSERM INST NAT SANTE RE.
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         Claim 8; page 21; 24pp; French.
                                                                                                                                                                                                                                                                                                                                      'HIV-1; AIDS; sense nucleotide;
                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Montagnier L;
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26; Conservative
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                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                 and HIV-1 Eli.
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acid amplification of conserved sequences of the gag, vpr, pol or vous genes of the HIV-1 strains Bru, Mal, Eli, HIV-2 ROD or simian immunodeficiency virus (SIV) MAC or the nef2, vif2 or vpx genes of HIV-2 ROD and SIV MAC. This primer is targetted to sequences in the env gene of the viral strains. The sequences are therefore used to detect HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer; PCR; amplification; gag; vpr; pol; vpu; HIV-1; HIV-2; SIV; nef2;
vif2; vpx; detection; ss.
                                                       amplification; gag; vpr; pol; vpu; HIV-1; HIV-2; SIV; nef2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The oligonucleotides AAT98010-T98059 are useful as primers for nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Human or simian immunodeficiency virus detection primer MMy8.
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                                                                                                                                                                                   Human immunodeficiency virus.
Simian immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Montagnier L;
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                                                                                           vif2; vpx; detection; ss.
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Best Local Similarity
Thes 26; Conserve
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6 15:35:22 2002

Fri Dec

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Gaps

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Indels

Length 27;

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This sequence represents a PCR primer for the simian immunodeficiency virus (SIV) gpl20 gene. The amplified sequence can be used in the chimeric virus of the invention. The chimeric virus is a chimeric SIV ppl20 gene. The chimeric virus is a chimeric SIV virus (SHIV) that infects macaque monkeys and causes them to develop AIDS-associated symptoms within 32 weeks, where the virus is generated by at least two passages of a SHIV containing DNA encoding HIV env protein through macaque bone marrow in vivo. The monkeys are useful as an animal model for HIV-1-induced disease.
                                    Chimeric SIV-HIV virus - for producing AIDS symptoms in macaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodefictency virus-1-HXB2 genome PCR primer ED12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodificiency virus type 1; HIV-1; HXB2 genome; PCR primer ED12; hetroduplex mobility assay; ss.
                                                                                                                                                                                                                                                                                                          100.0%; Score 26; DB 20;
100.0%; Pred. No. 0.00026;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                            Sequence 27 BP; 5 A; 11 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                      2 GTGCTTCCTGCTCCCCAAGAACCC 27
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                                                                                    Example; Column 13; 13pp; English.
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94US-0241373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                  26; Conservative
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WPI; 1999-069838/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The oligonucleotides AAT98010-T98059 are useful as primers for nucleic acid amplification of conserved sequences of the gag, vpr, pol or vpu genes of the HIV-1 strains Bru, Mal, Eli, HIV-2 ROD or simian immunodeficiency virus (SIV) MAC or the nef2, vif2 or vpx genes of HIV-2 ROD and SIV MAC. This primer is targetted to sequences in the env gene of the viral strains. The sequences are therefore used to detect HIV-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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(INSP ) INST PASTEUR.
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                                Simian immunodeficiency virus
                Human immunodeficiency virus.
                                                                                                                                       90EP-0401520.
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89FR-0007354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-2 or SIV infections.
                                                                                                                                                                                                                                                                                                          WPI; 1997-538622/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIND ( AIND)
                                                                                                                                   05-JUN-1990;
                                                                                                                                                                                         02-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-1995;
                                                                                                                                                                     20-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5849994-A.
                                                                  EP806484-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998
                                                                                                    12-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Narayan O;
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV08911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
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AA081320 and AA081321 (or AAQ81326) are a pair of primers for the first round PCR amplification of the human immunodeficiency virus-1-HXB2 genome. The primers were used in a hetroduplex mobility assay, to evaluate intra- and interpatient HIV sequence diversity.
                                                                                                                                                                                                                                                                                                                                                  sequence diversity - used to analyse sequence variation between genetic loci, and sequence diversity over time in samples serially obtd. from a single source
                                                                                                                                                                                                                                                                                                     Heteroduplex mobility assay for the analysis of nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30 BP; 7 A; 11 C; 6 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 26;
(STRD ) UNIV LELAND STANFORD JUNIOR. (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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New isolated HIV-1 group O strains - used to produce polynucleotides, antigens and antibodies for use in diagnosis and in vaccines for prevention of HIV-1 infection
                                                             HIV-1 group O; Outlier strain; 9941; envelope protein; antigen; vaccine; diagnosis; AIDS; PCR; primer; ss.
                                       HIV-1 group O gp41 region DNA primer 41-1.
                                                                                                           Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                              Example 1; Page 61; 162pp; English.
                                                                                                                                                                              98WO-EP04522.
                                                                                                                                                                                                      97EP-0870110.
              19-JUL-1999 (first entry)
                                                                                                                                                                                                                                                    Delaporte E, Peeters M,
                                                                                                                                                                                                                             (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                         WPI; 1999-132255/11.
                                                                                                                                WO9904011-A2
                                                                                                                                                                              20-JUL-1998;
                                                                                                                                                                                                      18-JUL-1997;
                                                                                                                                                        28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-AUG-2001
                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD07432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD07432/c
      δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducing a mucosal immune response to antigen-encoding DNA is improves by complexing the DNA to lipospermine (esp. DGGS, dloctadecylamidoglycylspermine) or lipospermidne which can facilitate transfection. Antigens are pref. viral envelope proteins, esp. HIV gphGo and its fragments. An immunisation construct DNAenv was prepared which encoded the HIV-1 envy protein. The construct was transfected into mice either as naked DNA or as a complex with BOGS. The persistence of DNAenv in tissues was determined by PCR analysis using primers EDS and ED12 (see AAT35933 and AAT35934) which amplify a fragment of 1200 bp from the HIV V3-V5 region. The presence of DOGS was shown to greatly improve transfection
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                         Rev response element; RRE; silent mutation; immunisation construct; mucosal response; transfection; lipospermine; lipospermidine; DOGS; dloctadecylamidoglycylspermine; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Inducing mucosal immune response by admin. of antigen-encoding DNA - complexed to lipo:spermine or lipo:spermidine, partic. for vaccination against HIV
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 30;
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
 Pred. No. 0.00026; ; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 100.0%; Score 26; DB 17; Similarity 100.0%; Pred. No. 0.00026; 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30 BP; 7 A; 11 C; 6 G; 6 T; 0 other;
                                   26
                                              56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GTGCTTCCTGCTCCCAAGAACCC 27
                                  1 GTGCTTCCTGCTGCTCCCAAGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 50; 82pp; English.
            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTGCTTCCTGCTGCTCCCAAGAACCC
100.0%;
                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                               95WO-US08374
                                                                                                                AAT35934 standard; DNA; 30
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX25184 standard; DNA; 34
             26; Conservative
                                                                                                                                                                                     HIV env PCR primer ED12.
                                                                                                                                                                                                                                                                                                                                                                            (UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-341965/34.
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                WO9621356-A1
                                                                                                                                                               25-FEB-1997
                                                                                                                                                                                                                                                                                                                              03-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                     13-JAN-1995;
                                                                                                                                                                                                                                                                                                      18-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                  Mitchell WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 efficiency
                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                       AAT35934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX25184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
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AAX25184/C
           Matches
                                                                                                     AAT35934
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Vanden Haesevelde M;

Saman E,

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This PCR primer, designated 41-1, is used as a sense primer in the PCR amplification of part of the gp41 region of HIV-1 group O or group M. Antisense primer 41-4 is given in AAX25185. Following the amplification, nested PCR can be performed using primers 41-6 (see AAX25186) and 41-7 (see AAX25187). The invention relates to new HIV-1 group O antigens (see AAX05546-625), including gp41 antigens, and the use of these antigens, or nucleic acids encoding them (see AAX25154-80), in the diagnosis and prophylaxis of AIDS. Vaccines that provide protective immunity against HIV-1 group O infection comprise or least one HIV-1 type O antigen, a nucleic acid encoding such an antigen, a virus-like particle comprising such an antigen, or an attenuated form of an HIV-1 type O strain. The invention also involving amplifying HIV-1 nucleic acids using a suitable primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic equivalent marker; cell quantification; real-time PCR; nucleic acid quantification; molecular beacon; thymocyte proliferation; T cell receptor; TCR; DNA deletion circle; thymic function; cancer; chemotherapy; radiotherapy; immune system disorder; HIV-1; pathogen; DiGeorge syndrome; congenital immunodeficiency disorder; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 26; DB 20;
100.0%; Pred. No. 0.00026;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34 BP; 7 A; 6 C; 15 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV-1 env gene amplifying forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTGCTTCCTGCTGCTCCCAAGAACCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 GTGCTTCCTGCTGCTCCCAAGAACCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD07432 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Matches 26; Conserv
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(first entry)

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Glycoprotein D; gD; recombinant antigen library; disease-related antigen; multivalent antigenic polypeptide production; infection; allergen; asthma; autoimmune disease; rheumatoid arthritis; diabetes; therapy; multiple sclerosis; inflammatory condition; cancer; contraception; immune response; PCR primer; ss.
                                                                                   PCR primer for HIV-1 gp120 coding sequence.
                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                         WO9941383-A1.
                                                 29-0CT-1999
                                                                                                                                                                                                                                                                                                           19-AUG-1999
                                                                                                                                                                                                                        Synthetic.
                 AAZ10963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of determining in a nucleic acid sample of cellular origin the number of copies per cell of a preselected polynucleotide target sequence, comprising quantifying at least one carget sequence, comprising quantifying at least one target sequence, one genomic equivalent marker sequence, and expressing the number of copies of the target sequence per cell as a ratio between comparison of the target sequence and that of the genomic equivalent marker sequence is performed using real-time PCR amplification using a forward primer, a reverse primer and a molecular beacon capable of binding to a subsequence within the target sequence and genomic equivalent compared primer and a molecular beacon capable of colluding to a subsequence within the target sequence and genomic equivalent marker sequence. The genomic equivalent marker may be used to identify other genetic sequences for use as genomic equivalent conting to the particularly useful in determining the number of copies of a markers. It is particularly useful in determining the number of copies of deletion circles which are useful in assessing thymic function.

CC Mesaurement of thymic function is an indicator of the ability of immune colls, e.g. chemotherapy or radiotherapy. This is useful conting the course of diseases and therapies directed to diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involving immune system e.g. HIV-1 infection, congenital immunodeficiency disorder e.g. DiGeorge syndrome, and iatrogenically-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunodeficient states, e.g., by chemotherapy or radiotherapy for treatment of dysproliferative diseases e.g. cancer, and in bone marrow transplant. The method is also useful in determining number of genomes and cells in a biological sample, monitoring thymic function with age, idetermining target sequences of a pathogen or infectious particles e.g. viruses, bacteria, fungi and parasites on a per cell basis. Examples of viral DNA sequences that can be quantified are HIV-1 proviral DNA (gag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              per cell basis.
                                                                                                                                                                                                                                                                                                                      Determining the number of copies per cell of a preselected polynucleotide target sequence, for monitoring immune system recovery, comprises quantifying at least one target sequence and at least one
dysproliferative disease; bone marrow transplant; infectious particle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1 (HIV-1) env gene amplicon
was used for assaying abundance of HIV-1 provirions on a per c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and env regions) and human herpes virus 8 (HHV-8) ORF25 The present sequence is a PCR primer used to amplify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 C; 8 G; ...
88.5%; Score 23; DB 22; Le
... α. Pred. No. 0.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 6 A; 5 C; 8 G; 5 T; 0 other;
                                                                                                                                                                                                                                                         HO DD;
                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Column 29-30; 26pp; English.
                                               Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                             genomic equivalent marker sequence
                                                                                                                                                                                                                                                        Lewin SR, Kostrikis L,
              HIV-1; env gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIGCTICCTGCTGCTCCCAAGAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 GTGCTTCCTGCTCCCCAAGAA 1
                                                                                                                                                    11-JAN-2000; 2000US-0481288.
                                                                                                                                                                                      99US-0115432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                        WPI; 2001-366408/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 23; Conserv
                                                                                 US6235504-B1.
                                                                                                                                                                                      11-JAN-1999;
                                                                                                                   22-MAY-2001
                                                                                                                                                                                                                                                         Zhang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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οy
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This sequence represents a PCR primer for DNA encoding the HIV gpl20 coding sequence. The amplified sequence was used to create a recombinant antiquent library. The library comprises recombinant nucleic acids encoding antigent polypeptides and is produced by recombination of at least two forms of nucleic acid, differing by at least two nucleotides, encoding a disease related antigenic polypeptide. The library can be used to produce a recombinant multivalent antigenic polypeptides of the invention, that contains at least two antigenic polypeptides of the invention, that contains at least two antigenic polypeptides are used in vaccines to induce a protective or therapeutic response to a wide variety of infectious agents (bacteria, viruses, parasites, including plasmodium falciparum); allergens; asthma; autoimmune disease (e.g. rheumatoid architis, diabetes, multiple sclerosis); other inflammatory conditions and cancer, also, where directed against sperm antigens they can be used for contraception. The multivalent peptides can be evolved to induce an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     optimised immune response against a wide variety of antigens, particularly a broad spectrum response to many different strains of pathogen, including strains that are likely to appear in the future.
                                                                                                                                                                                                                                                                                                                                                                                               Recombinant multivalent antigenic polypeptide produced by recombining nucleic acid sequences and screening, used in vaccines against e.g. infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 20; Length 25;
Pred. No. 0.009;
                                                                                                                                                                                                                                                                     Stemmer WPC, Whalen RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 6 A; 11 C; 3 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Fig 8b; 153pp; English.
                                                                                                                                                                                                                                                                         Punnonen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCCTGCTGCTCCCAAGAACCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTTCCTGCTGCTCCCAAGAACCC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
                                                                                              98US-0021769.
98US-0074294.
                                                                  98US-0105509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.5%;
99WO-US02944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ40104 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                         Bass SH, Howard R,
                                                                                                                                                                                                      (MAXY-) MAXYGEN INC.
                                                                                                                                                                                                                                                                                                                                       WPI; 1999-518452/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
   10-FEB-1999;
                                                                  23-OCT-1998;
                                                                                                                                    11-FEB-1998;
                                                                                                        1-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ40104;
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ID AAQ4
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AAZ10963 standard; DNA; 25 BP.

RESULT 10 AAZ10963 ID AAZ1

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New HIV and envelope glycoprotein mutant(s) - comprising an antibody-dependent enhancing domain with an amino acid alteration, for use in vaccines and immunogenic compositions
                                                                                                                                                                                                                                               The present sequence was used in the development of a novel HIV comprising an antibody-dependent enhancing (ADE) domain, which contains at least one amino acid alteration.

The virus can be used in vaccines or immunogenic compositions to prevent or reduce the induction of enhancing antibodies, while maintaining the capacity to induce or bind protective or meutralising antibodies. In particular, it can be used to induce a mucosal immune response to HIV. It can also be used to evaluate immune responses and compounds which affect such responses.
                                                                                                                                                                                                                                                                                                                                                                                                               80.8%; Score 21; DB 19; Length 29; 100.0%; Pred. No. 0.097; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29 BP; 7 A; 11 C; 6 G; 5 T; 0 other;
                                                                                                                                                                                                                         Example; Page 56; 102pp; English.
                                                       96US-0021668.
                              97WO-US11667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TCCTGCTGCTCCCAAGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                   (UYVA-) UNIV VANDERBILT
                                                                                                                                        WPI; 1998-110233/10.
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Best Local Similarity
Matches 21; Conserv
                              02-JUL-1997;
                                                       05-JUL-1996;
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01-SEP-1995;
                                                                                                              Mitchell WM;
 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                            Since tat and rev are able to transactivate HIV gene expression and are essential for viral replication, two oligomers, rev-1 and rev-2 complementary to these overlapping reading frames were synthesised. Rev regulates HIV gene RNA expression through interaction with the rev-response element (RRE). The synthetic oligomer RRE was directed against the RRE target sequence at the site of overlap with the rev binding site. The antisense oligonucleotide can be used to treat HIV-I and its use prevents the formation of escape mutants of the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                Human immunodeficiency virus; anti-viral drugs; in vivo; screening; antisense oligonucleotides; target; ss; rev-response element.
                                                                                                                                                                                                                                                                                                                                            Cell culture system for evaluating antiviral drug treatment - comprises long term culture which allows prodn. of escape mutants \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer; HIV; DNAenv; V3-V5 region; vaccine; antibody-dependent enhancing domain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28 BP; 5 A; 11 C; 5 G; 7 T; 0 other;
                                                    RRE oligonucleotide from the HIV genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer ED12 for HIV DNAenv V3-V5 region.
                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 GIGCITCCIGCIGCICCCAAGA 28
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            (updated)
(first entry)
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22; Conservative
                                                                                                                                                                                                                                                                                        Lisziewicz J, Sun DMS;
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                                                                                                                                                   JSN7906881-N.
                                                                                                                                                                                                        02-JUL-1992;
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           17-DEC-2001
23-AUG-1993
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                                                                                                                        Synthetic.
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Gaps

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26

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Selenoprotein; HIV; Ebola virus; cancer; immune system disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New selenoprotein for use in detecting certain viruses, e.g. human immunodeficiency virus (HIV) or Ebola, cancer and immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nadimpalli RG, Ramanathan CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 12C; 140pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                               Pseudoknot oligonucleotide #19.
6 TCCTGCTGCTCCCAAGAACCC 26
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AAX22363;
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        The present invention relates to selenoproteins encoded in the genome of a virus, where the coding sequence of the selenoprotein is genetically engineered for expression in a nucleic acid construct. The invention also discloses a method for identifying selenoprotein coding sequences, for detecting certain viruses (e.g. HIV or Ebola), cancer and immune system disorders. The present sequence was used to illustrate the invention.
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                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                     Human immunodeficiency virus; HIV; antigen; detection; diagnosis;
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                                                                                          Score 21; DB 24; Length 38;
Pred. No. 0.097;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              retrovirus; vaccine; lymphocyte; reverse transcriptase; amplification; primer; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deriv. cDNA or antigens, useful for diagnosing retroviral infections and vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New HIV-type immune deficiency virus ECACC V 92092318 -
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100.0%; Pred. No. 0.32;
iive 0; Mismatches 0
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                                                                           Sequence 38 BP; 6 A; 6 C; 14 G; 12 U; 0 other;
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                                                                                                    100.0%; Preu. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 5; 73pp; German.
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                                                                                                                                                                                                      AAQ58958 standard; DNA; 24 BP
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92DE-4235718.
92DE-4244541.
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                                                                                              80.88;
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                                                                                                                                              38 TCCTGCTCCCAAGAACCC
                                                                                                                                    6 TCCTGCTGCTCCCAAGAACCC
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                                                                                             Query Match 80.8
Best Local Similarity 100.
Matches 21; Conservative
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30-DEC-1992;
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Matches
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                                                                                                                                                                                                                  assay kit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                  HIV-type retrovirus; MVP-5180/91; ECACC V 92092318; antigen; detection; antibody; immune deficiency; vaccine; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%; Score 20; DB 20; Length 24; 100.0%; Pred. No. 0.32; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DADE-) DADE BEHRING MARBURG GMBH.
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  BP.
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92DE-4233646.
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AAX22363 standard; DNA; 24
                                                                                                       19-MAY-1999 (first entry)
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Best Local Similarity
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22-OCT-1992;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

Note		מו וווסמפד
0-105-51 CCTGCTGCTCCCAAGAACCC 26 C. 0 , Gapext 60.0 seqs, 14551402878 residues seqs, 14551402878 residues seqs, 14551402878 residues lifying chosen parameters: 0 first 45 summaries first 45 summaries i* tg;* n: tg;* n: tg;* n: tg;* n: thin: hum: thin: hum: thin: thin	on: December 5, 2002, 21:54:08; Sear (withou 442.731	; Search time 1709.1 (without alignments) 442.731 Million cell
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Pred. No. is the number of results predicted by chance to have a

linear PAT 08-JUL-1996

DNA

ALIGNMENTS

A31980 26 bp D Synthetic HIV-1/2 diagnosis primer. A31980 A31980.1 GI:1567263

RESULT 1
A31980
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM

synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 26)
Moncany, M. and Montagnier, L.
Nucleotide sequences of retroviral genomes of types HIV-I, HIV-2
and SIV, their uses for the amplification of these genomes and
diagnosis in vitro of these viral infections

REFERENCE AUTHORS TITLE

Result No.		ď			SUMMARIES	
1 1	Score	ت ن	Ä	DB	ΩI	Description
	26	100.0	56	٠٠	A31980	A31980 Synthetic H
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11	20		24	9	A38027	A38027 Sequence 34
12	20	76.9	24	9	AR059451	AR059451 Sequence
13	20		24	9	AX001384	Segue
14	20	76.9	24	9	BD000313	BD000313 CDNA COMP
15	19	73.1	36	9	AR017599	AR017599 Sequence
16	19		36	Q	AR068245	AR068245 Sequence
17	18	69.5	18	9	AR017596	AR017596 Sequence
18	18		18	9	AR068242	42 Sequenc
	18	69.2	40	9	A38020	Seq
c 20	18		40	<u>ه</u> ا	AR017597	AR017597 Sequence
	18	69.2	40	9	AR059444	AR059444 Sequence
C 55	18		40	۰ م	ARU68243	AR068243 Sequence
233	18		40	، م	AX001377	Sedne
	18		40	، م	BD000306	
	17		21	9	AX472697	AX472697 Sequence
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	15	57.7	20	9	A24306	SK68
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Moncany, m. and Montagnier, L.
Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
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Hes 26; Conservative 0; Mismatches 0;
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JP 2000093187-A/51.
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Monoany, M. and Montagnier, L.
Monoany, M. and Montagnier, L.
Mucleotide sequences derived from the genome of retroviruses of the
HIV-1, HIV-2, and SIV type, and their uses in particular for the
amplification of the genomes of these retroviruses and for the in
vitro diagnosis of the diseases due to these viruses
Patent: US 6194142-A 51 27-FEB-2001;
Location/Qualifiers
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artificial sequences.

1 (bases 1 to 26)
Moncany,M. and Montagnier,L.
Nucleotide sequences of retroviral genomes of types HIV-I, HIV-2
and SIV, their uses for the amplification of these genomes and
diagnosis in vitro of these viral infections
Patent: EP 0403333-A 36 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
Patent: EP 0403333-A 35 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
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ilarity 100.0%; Pred. No. 4.2e-05;
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/organism="synthetic construct"
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NO 47-LIMICIALS SEQUENCE

PD 04-APR-2000

PF 24-SEP-1999 UP 1999270165

PR 02-JUN-1899 FR 89/07354,20-SEP-1989 FR 89/12371 PI

MAURICE MONCANY, LUC MONTAGNIER

PC C12NIS/509, A61K39/21, A61K48/00, A61P31/18, C07H21/04, C07K14/155,

PC C12OL/68, C12O1/70, G01N33/569, C12NIS/00

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Location/Qualifiers

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JP 2000093187-A/52.
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artificial sequences.
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Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
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Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
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llarity 100.0%; Pred. No. 4.2e-05;
Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/db_xref="taxon:32630"
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Best Local Similarity 100.0%; P
Matches 26; Conservative 0;
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Matches 26; Conserv
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BD001805/c
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AR066367
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Unclassified.

1 (bases 1 to 24)

Zhang,L., Lewin,S.R., Kostrikis,L. and Ho,D.D.
Methods for identifying genomic equivalent markers and their use in quantitating cells and polynuclectide sequences therein
Patent: US 6235504-A 23 22-MAY-2001;
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Vanden, H.M. and Saman, E.
HIV-1 GROUP O ANTIGENS AND USES THEREOF
Patent: WO 9904011-A 139 28-JAN-1999;
VANDEN HAESEVELDE MARLEEN (BE); INNOGENETICS NV (BE)
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100.0%; Score 26; DB 6; ilarity 100.0%; Pred. No. 4.2e-05; Conservative 0; Mismatches 0;
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Pred. No. 4.2e
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Sequence 23 from patent US 6235504.
ARI55415.
ARI53415.1 GI:15120947
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    .34
    /organism="unidentified"

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BDU00313 24 bp DNA linear PAT 31-JAN-2002 CDNA complementary to RNA of immunodeficiency virus of hiv group. BD000313
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Guerller, L. G., Eberle, J., Brunn, Av., Knapp, S. and Hauser, H.-P. Retrovirus from the HIV group and its use Patent: US 5840480-A 34 24-NOV-1998;
Location/Qualifiers
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1 (bases 1 to 24)
Guertler, L. G. and V, B. A.
Retrovirus of the HIV-group and its application
Patent: EP 0890642-A 34 13-JAN-1999;
DADE BEHRING MARBURG GMBH (DE)
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AR059451
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Sequence 34 from Patent EP0890642.
AX001384.1 GI:7241558
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/organism="unidentified"
/db_xref="taxon:32644"
a 10 c 5 g
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10 c 5 g
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Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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JP 2000312592-A/34.
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BD000313
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AX001384
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AR059451
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(Inclassified. 10.38)

Taylor,E.Will., Nadimpalli,R.Gopal. and Ramanathan,C.Sekar. Selenoproteins. coding sequences and methods
Patent: US 6303295-A 32 16-0CT-2001;
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Guertler,L.G., Eberle,J.D., Brunn,V.A., Dr, Knapp,S.D. and
Hauser,H.D.
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                          Length 24;
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                          Score 23; DB 6; Le
Pred. No. 0.0028;
0; Mismatches 0;
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Pred. No. 0.046;
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Sequence 32 from patent US 6303295.
AR172210. GI:17911701
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Sequence 34 from Patent EP0591914.
A38027
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/db_xref="taxon:32644"
10 c 5 g 3
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6 c 14 g
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100.0%; Pre
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AR172210/c
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synthetic construct
artificial sequences.

1 (bases 1 to 24)

2 (burutora, L.G., Evelre, J., Brunne, A.F., Knapp, S. and Hauser, H.P.

CDNA complementary to RNA of immunodeficiency virus of hiv group

BIDDO BEOHRING MARUBURUG GMBH

OS Artificial Sequence

PN D 2000312592-A34

PN D 2000312592-A34

PN 14-NOY-2000

PF 23-FEB-2000 JP 2000045665

PR 23-FEB-2000 JP 2000045665

PR 06-OCT-1992 DE P4235646.5,22-OCT-1992 DE P4318186:4 PI LUTZ GGRUTORA, JOSEPH RYGER, ALBRECHT FAU BRUNNE, PI STEPHEN KNAPP,

PT HANS PATER HAUSER

PC C12N15/09, C07K14/155, C12N7/00, C12Q1/68, G01N33/569//A61K39/21,

PC A61P31/18,

PC C12N15/00

CC FH Key

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//organism-'Artificial Sequence'.
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1 (bases 1 to 36)
Sheridan, P.J., Gagne, J.C. and Anderson, M.L.
Oligonucleotide probe conjugated to a purified hydrophilic alkaline phosphatase and uses thereof
Patent: US 5780227.
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/organism="synthetic construct"
/db_xref="taxon:32630"
a 10 c 5 g 3 t
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Pred. No. 0.77;
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Sequence 5 from patent US 5780227.
AR017599.1 GI:3973202
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6 a 9 c 9 g
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Best Local Similarity 100.
Matches 19; Conservative
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AZ793609 2M0047B02
AZ366164 1M0115H20
BH864943 SALK_0971
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AA873218 oh70f08.s
AI810043 wf79f06.x
AZ804486 ZM0055D07
AI338567 qq98f04.x
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AI47308 tmm27a05.x
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to S0)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hat,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
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Institute of Medical Science, University of Tokyo
4-6-1, Elizirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
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Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers

FEATURES

AZ762628 IM0557A16 AL461090 T. brucei BH864584 SALK_0962 AU106268 AU106268 AZ795136 2M0049A16

AZ762628 TA89E09P BH864584 AU106268 AZ795136

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Direct Submission

Libration (10-DEC-2000) Trypanosoma brucel genome sequencing project. Submission

Eubmitted (10-DEC-2000) Trypanosoma brucel genome campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk and constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelssyed@tigr.org

betails of T. brucei sequencing at the Sanger Centre are available at http://www.sanggar.ac.uk/Projects/T_brucei/.
  of pWD42 (gil4732114|gb|AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and solected for ampicillin resistance."
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1 (bases 1 to 40)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were lighted to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
                                                                                                                                                                                                                                                                                                                                                                                                                                             1M0557A16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0557A16 R, DNA sequence.
AZ762628
AZ762628.1 GI:12872834
GSS.
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              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ColrF0073"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
a 9 c 17 g 7 t
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42ry: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                  Length 50;
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100.0%; Pred. No. 1.1e+04;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0557 row: A column: 16
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seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
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/organism="Mus musculus"
/strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIMO557A16"
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Fax: 801 585 7177
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/clone="SALK_096296"
/clone="SALK_096296"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of Which contains one or more TDNA insertion
elements. The resultant fragment for each line was a
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
19 c 2 g 17 t
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A Sequence-Indexed Library of Insertion Mutations in the
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Arabidopsis thaliana
Bukaryota; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 48)
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1 (Jases 1 to 50)
Suzukl,Y., Tana,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hat,Y., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Namanura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
Contact: Yutaka Suzuki
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AU106268 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS11437, mRNA sequence.
SALK_096296 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_096296, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Far: 858 453 4100 x1752
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100.0%; Pred. No. 3.7e+04;
Live 0; Mismatches 0;
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ВН864584.1 GI:22100482
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AU106268.1 GI:13555789
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                                                                                                                                                                                                                                                                                                                       Arabidopsis Genome
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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2M0049A16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0049A16 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethyliumarate treated 0937 cells"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS11437"
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Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC2M0049A16"
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor object of the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agances gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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/organism="Mus musculus"
/strain="c57BL/60"
/db.xref="taxon:10090"
/clone="UUGCIM0013G17"
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Insert Length: 10000 Std Error: C
Plate: 0013 row: G column: 17
Seg primer: CACACAGGAAACAGCTATGACC
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High quality sequence stop: 23.
Location/Qualifiers
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AZ309461.1 GI:10350466
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Best Local Similarity 100.0
These 10; Conservative
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Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 27)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.
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/clone="UGGC2M0142006"
/clone_lib="Mouse 10kb plasmid UUGClM library"
/sex="Male"
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Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: O column: 06
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

    27
    /organism="Mus musculus"
    /strain="C57BL/6J"

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University of Utah Genome
University of Utah
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AZ843637.1 GI:13013545
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Unpublished (2000)
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Fax: 801 585 7177
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Gaps

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(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
                                                                              constructed by Bento Soares and M. Fatima Bonaldo.  6 \ c \  \  \, 5 \ g \  \  \, t \  \  \, 
                                                                                                                                                                       ch 43.5%; Score 10; DB 9; Length 28; 1 Similarity 100.0%; Pred. No. 1.1e+05; 10; Conservative 0; Mismatches 0; Indels
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Matches 10; Conser
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AI810043/c
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymuclectide kinse. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into capacity competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (1997)

Unpublished (1997)

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmail: procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E., Consortium/LLNL at:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_nost="DH108"
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/db_xref="taxon:9606"
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Best Local Similarity 100.0
Matches 10; Conservative
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REFERENCE

FEATURES

RESULT 9 AA873218

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/dec="Orger and possible to the control of the cont
              EST 19-DEC-1999
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I (bases 1 to 20)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
AI810043 28 bp mRNA linear EST 19-DEC-19
wf79f06.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2361827 3' similar to TR:060281 060281 KIAA0530 PROTEIN ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 746 Std Brror: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                  AI810043.1 GI:5396609
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Unpublished (1997)
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DEFINITION ACCESSION VERSION

RESULT 11 AZ804486

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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...., Jay DNA linear GSS 16-FEB-2001
IN0584F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0584F04 R, DNA sequence.
                                                          AI338567 31 bp mRNA linear EST 13-FEB-1999 qq98f04.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1939423 3' similar to TR:Q66660 Q66660 ORF 58. ;, mRNA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Longarcer, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1382 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/clone="InAnGE:1939423"
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/lab_host="DH108"
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100.0%; Pred. No. 1.1e+05;
iive 0; Mismatches 0;
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/organism="Homo sapiens"
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AI338567.1 GI:4075494
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nes 10; Conservative
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                               AI338567/c
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AZ773199
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RESULT 12
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Elamama, Elama
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                                                          A2804486 30 bp DNA linear GSS 16-FEB-2001
2M0065D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0065D07 F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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/strain="c57BLf6]"
/db_xref="taxon:10090"
/clone="UGC2M0065D07"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 43.5%; Score 10; DB 17; Length 30; I Similarity 100.0%; Pred. No. 1.1e+05; 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: D column: 07
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
                                                                                                                                                                  AZ804486
AZ804486.1 GI:12956809
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                    house mouse.
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USA
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source

FEATURES

BASE COUNT

Matches

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us-09-670-105-48.oli.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (glif47321141gbjAR129072.1). a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Eukaryota: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                             Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Milyersity of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
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IMAGE:2157776 3' similar to SW:Y273_HUMAN Q92561 HYPOTHETICAL
PROTEIN KIAA0273. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC2M0067L07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: L column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
/strain="C57BL/6J"
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Location/Qualifiers
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A1479308.1 GI:4372476
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                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
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Best Local Similarity
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AI479308/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
//ab_host="E. Coli strain XI10-Gold, T1-resistant, F-"
//ab_host="E. Coli strain XI10-Gold, T1-resistant, F-"
//note="Vector: PWD42DY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
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Dunn,D., Aoyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A2805966 34 bp DNA linear GSS 20-FEB-20C 2M0067L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0067L07 R, DNA sequence.
                        plasmid inserts
(hobblished (2000))
Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
Rm. 108, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
  Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Emall: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                        Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .34 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0584P04"
                                                                                                                                                                                                                                                                                                             0584 row: P column: 04
                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 34.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A2805966.1 GI:12966777
                                                                                                                                                                                                                                                                                                                                                                      Class: plasmid ends
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Matches 10; Conservative
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Gaps ö

0; Indels

à g EST 14-APR-1999

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mRNA

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1. 37
/organism="Homo sapiens"
/db_raref="texaon:9606"
/clone="InAGE:215776"
/clone="InAGE:215776"
/clone="InbaGE:215776"
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/lab_host="DH108"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH139W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 ilbraries. The pools consisted of I.M. A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capabs-refmail.nih.gov
This clone is available royally free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1042 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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Search completed: December 6, 2002, 00:45:08 Job time: 1428.53 secs

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Gaps ó;

0; Indels

43.5%; Score 10; DB 9; Length 37; 100.0%; Pred. No. 1.2e+05; Live 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.

14 CAGAAGAAGA 23 ·21 CAGAAGAAGA 12

δ g

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TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Sequence 95, Appl
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19, 7
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/cgn2_6/ptodata/1/ina/5B_COMB.seg:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-051-446-4
US-08-414-019A-3
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US-09-324-867-52
US-09-091-058-18
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                                                                                                                                                                                                       1 AATGGCAGTCTAGCAGAAGAGA 23
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                                                                nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Perfect score:
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APPLICANT: Moncany, Maurice
APPLICANT: Moncany, Maurice
APPLICANT: Moncany, Maurice
APPLICANT: Moncany, Maurice
TITLE OF INVENTION: Nuclectide Sequences Derived From The
TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The
TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosi
TITLE OF INVENTION: Of The Diseases Due To Those Viruses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
     sednence sed
       Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
US-09-109-063-36
US-09-109-063-37
US-09-10-058-119
US-08-242-664-24
US-08-08-138-24
PCT-US95-06379-24
US-08-088-658-39
US-08-08-658-39
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US-08-150-156A-32
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US-08-373-124A-594
US-08-373-124A-596
US-08-373-124A-596
US-08-373-124A-598
US-08-373-124A-598
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US-08-373-124A-1631
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APPLICATION NUMBER: US/08/472,928
FILING DATE: 07-UNV-1995
APPLICATION NUMBER: US 08/160,465
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APPLICATION NUMBER: US/09/092,07
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8912371
FILING DATE: 20-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8907354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/09092077 Patent No. 6194142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 023
TELECOMMUNICATION:
TELEPHONE: (202)408-4000
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TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 2; Length 42; 100.0%; Pred. No. 0.00082; Ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IEMPC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDEREET 5.1
CURRENT APPLICATION DAYA:
PILING DATE: 26-OCT-1994
CLASSIFICATION NUMBER: US/08/050,478
FRICASSIFICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US OF 868,747
FILING DATE: 27-MAR-1992
CLASSIFICATION NUMBER: US OF 868,747
FILING DATE: 27-MAR-1992
CLASSIFICATION NUMBER: US OF 868,747
REGISTRATION 1938
REGISTRATION NUMBER: 34,398
REGISTRATION NUMBER: 34,398
REGISTRATION NUMBER: 34,398
                                                                                                                                                                                                                                                           Sequence 95, Application US/08050478 Patent No. 5972596 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 95, Application US/09414117
Patent No. 6291664
GENERL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                       1 AATGGCAGTCTAGCAGAAGA 23
                                                                                                 13 AATGGCAGTCTAGCAGAAGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AATGGCAGTCTAGCAGAAGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212)758-4800
TELEFRAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 95
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 345 PARK AVENC
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 42 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                            RESULT 3
US-08-050-478-95
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US-08-050-478-95
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US-09-414-117-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                           100.0%; Score 23; DB 4; Length 23; ilarity 100.0%; Pred. No. 0.00085; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 42;
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100.0%; Score 23; DB 2; PBest Local Similarity 100.0%; Pred. No. 0.00082; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NEW IOAN

COUNTRY: USA

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: ELOPPY DISK
COMPUTER: IBM PC COMPATIBLE
CORFACTION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,049
FILING DATE: 20-027-1997
FILING DATE: 26-027-1994
CLASSIFICATION NUMBER: US 08/050,478
FILING DATE: 29-MAR-1993
CLASSIFICATION NUMBER: US 08/050,478
FILING DATE: 29-MAR-1993
CLASSIFICATION NUMBER: US 08/050,478
FILING DATE: 29-MAR-1993
CLASSIFICATION NUMBER: US 07/858,747
FILING DATE: 29-MAR-1992
CLASSIFICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION NUMBER: 2026-4006USI
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFRANE: (212)751-6849
TELEFRANE: WART J. TELEPHONE: (212)751-6849
TELEFRANE: CHARACTERISTICS:
TENENGE: CHARACTERISTICS:
TENENGE: WATTONENGENERE
CONTINUED THE CATTONENGENERE
TELEPHONE: (212)751-6849
TELEFRANE: WATTONENGENERE
TELEPHONE: AND TONES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-850-049-95; Sequence 95, Application US/08850049; Sequence 95, Application US/08850049; Patent No. 5665726; GENERAL INFORMATION:
LENGTH: 23 base pairs;
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-092-077-48
                                                                                                                                                                                                                                                                                                                                                                      1 AATGGCAGTCTAGCAGAAGAAGA 23
                                                                                                                                                                                                                                                                                                                                            1 AATGGCAGTCTAGCAGAAGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: MORGAN & FINNEGAN
345 PARK AVENUE
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STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-850-049-95
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Gaps

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100.0%; Score 23; DB 4; Length 42; 100.0%; Pred. No. 0.00082;
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APPLICANT: James McSwiggen
APPLICANT: Dan T. Stinchcomb
APPLICANT: James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                   PRICATION NUMBER: US/09/678,437
FILING DATE: 02-0ct-2000
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/850,049
FILING DATE: 40R00wn>
APPLICATION NUMBER: US/0858,747
FILING DATE: 29-WAR-1993
APPLICATION NUMBER: US 07/858,747
FILING DATE: 29-WAR-1993
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-WAR-1993
APPLICATION NUMBER: US 07/858,747
FILING DATE: 37-WAR-10N:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 2026-4006US1
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    including appplication described below:
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  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: LINEAR
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTEMOVERSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/271,880A FILING DATE: July 7, 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including appropries application DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 183, Application US/08271880A Patent No. 5693535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 95: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AATGGCAGTCTAGCAGAAGAAGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 42 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
APPLICANT: Bharat Chowrira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Conservative
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STATE: California
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Matches 23; Conserva
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US-08-271-880A-183
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GENERAL INFORMATION:
APPLICANT: «Unknown»
TITLE OF INVENTION: METHOD OF ELIMINATING
INTERIAL OF INVENTIONS OF MRNA
TITLE OF INVENTION: METHOD OF ELIMINATING TITLE OF INVENTION: INHIBITORY/INSTABLLITY REGIONS OF MRNA NUMBER OF SEQUENCES: 130 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 100.0%; Score 23; DB 4; Length 42. Length 42. L. Similarity 100.0%; Pred. No. 0.00082; 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
REFERENCE/DOCKET NUMBER: 21206-4006US1
TELECHOME: (212)758-4800
TELEPHONE: (212)758-4800
                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,117
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/US93/02908
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 95, Application US/09678437
; Patent No. 6414132
                                                                                          ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AATGGCAGTCTAGCAGAAGAAGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 95: SEQUENCE CHARACTERISTICS: LENGTH: 42 BASE PAIRS
                                                                                                             STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                       10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-414-117-95
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US-09-678-437-95
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James McSwiggen
Dan T. Stinchcomb
James D. Thompson
James D. Thompson
James D. Thompson
HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                     Score 20; DB 2;
Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELER: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: IBM P.C. DOS 5.(
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/910,408
FILING DATE: CURNOWN>
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-09-249-215-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 183, Application US/09249215
Patent No. 6159692
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kenneth G. Draper
Bharat Chowrira
                                                                                                                                                                                                                                          э;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 183:
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STRANDEDNESS: single
                                                                                                                                                                                                   87.0%;
85.0%;
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  3 TGGCAGTCTAGCAGAAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 232
                  TELEX: (7-31)
TELEX: (7-310)
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLIGY: linear
US-08-910-408-183
      (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071
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        TELEFAX:
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Fatent No. 5972704
GENERAL INFORMATION:
APPLICANT: Bharat Chowrira
APPLICANT: Dan T. Stinchomb
APPLICANT: Dan T. Stinchomb
APPLICANT: James McSwiggen
APPLICANT: James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 20; 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB Pred. No. 0.033; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,408
                                                                                               NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 206/116
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: MAY 14, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,880
FILING DATE: July 7, 1994
APPLICATION NUMBER: 08/103,243
FILING DATE: AUGUST 6, 1993
APPLICATION NUMBER: 07/882,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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85.0%;
                                                                                                                                                                        TELEFAX: (212,
TELEFX: 67.3510
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 UGGCAGUCUAGCAGAAGAAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · 3 TGGCAGTCTAGCAGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: SI

TOPOLOGY: linear

US-08-271-880A-183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 1; Length 31;
Pred. No. 0.1;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Finnegan, Henderson, Farabow, Garrett E: Dunner
1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,770
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                       05495-0001-00000
                APPLICATION NUMBER: DE P 42 33 646.5 FILING DATE: 06-OCT-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE P 42 35 718.7 FILING DATE: 22-OCT-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE P 42 44 541.8 FILING DATE: 30-DEC-1992 PRIOR APPLICATION NUMBER: DE P 42 18 186.4 FILING DATE: 01-JUN-1993 ATTONENY GENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: DE P 42 33 646.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-471-770-25
; Sequence 25, Application US/08471770
; Patent No. 5770427
                                                                                                                                                                                                                                                                                        NAWE: Michael J. Blake
REGISTATION NUMBER: 37,096
REFERENCE/DOCKET NUMBER: 0549;
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-408-4400
TELEFAN: 202-408-4400
INFORMATION FOR SEQ ID NO: 25:
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100.0%; Pr
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APPLICANT: Guertler, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Brun, Albrent v.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-470-202-25
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05-0CT-1993
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA ZIP: 20005 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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ADDRESSEE:
STREET: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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Sequence 19, Application US/08722015A

Sequence 19, Application US/08722015A

Sequence 19, Application US/08722015A

Sequence 19, Application US/0881

GENERAL INFORMATION:

APPLICANT: Fouchier, Ronaldus A.M.

APPLICANT: Schuitemaker, Johanna

TITLE OF INVENTION: INDUCING AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN IMMUNC

TITLE OF INVENTION: INDUCING AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN IMMUNC

TITLE OF INVENTION: 105/08/722,015A

CURRENT RILING DATE: 1996-11-19

NUMBER OF SEQ ID NOS: 258

SOFTWARE: Patentin version 3.1

SEQ ID NO 19
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Patent No. 5759808
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
APPLICANT: Brunn, Albrecht v.
APPLICANT: Rauge, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Netrovirus from the HIV Group and Its
TITLE OF INVENTION: Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.0%; Score 20; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 0.031; Matches 20; Conservative 0; Mismatches 0; Indels
                87.0%; Score 20; DB 3; Length 20;
85.0%; Pred. No. 0.031;
tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finnegan, Henderson, Farabow, Garrett & Dunner
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic Oligonucleotide US-08-722-015A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGGCAGTCTAGCAGAAGAAG 20
                                                                                                           3 TGGCAGTCTAGCAGAAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TGGCAGTCTAGCAGAAGAAG 22
                                                                                                                                                   1 UGGCAGUCUAGCAGAAGA 20
              Query Match
Best Local Similarity 85.03
Matches 17; Conservative
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ADDRESSEE: Finnegan,
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20002
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US-08-470-202-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Guertler, Lutz G.
APPLICANT: Berle, Josef
APPLICANT: Berle, Josef
APPLICANT: Berle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
TITLE OF INVENTION: RETROVINUS FROM HIV GROUP AND ITS USE
FILE REPERBNCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/109,916
CURRENT APPLICATION NUMBER: DP 42 33 646.5
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1992-10-06
EARLIER FILING DATE: 1992-10-22
EARLIER APPLICATION NUMBER: DE P 42 44 541.8
EARLIER FILING DATE: 1992-12-30
EARLIER FILING DATE: 1992-12-30
EARLIER FILING DATE: 1993-10-22
EARLIER FILING DATE: 1993-10-23
EARLIER FILING DATE: 1993-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 31; 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.6%; Score 19; DB 4; Length 31; llarity 100.0%; Pred. No. 0.1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                   NAME: Carol P. Einaudi
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 05495-0001-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHRACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.6%; Scor.
100.0%; Pred. No. v.
                                                                                             FILING DATE: 30-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                DE P 42 44 541.8
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US-09-109-916-25
; Sequence 25, Application US/09109916
; Patent No. 6277561
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-059-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GGCAGTCTAGCAGAAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GGCAGTCTAGCAGAAGAAG 31
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 31
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Best Local Similarity 100.
Matches 19; Conservative
                                 FILING DATE: 22-OCT-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 19; Conserv
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| Patent No. 5840480
| GENERAL INFORMATION:
| APPLICANT: Guerler, Lutz G. APPLICANT: Berle, Josef
| APPLICANT: Brunn, Albrecht v. APPLICANT: Knapp, Stefan
| APPLICANT: Knapp, Stefan
| APPLICANT: Hauser, Hans-Peter
| TITLE OF INVENTION: Retrovirus from the HIV Group and Its ITLE OF INVENTION: Use
| NUMBER OF SEQUENCES: 63 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STERET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 31; 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/468,059
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 01-JUN-1993
ATORNEY/AGENT INFORMATION:
NAME: CAPLI P. EINAUTI
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 32,220
TELECHMONICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPHONE: 202-408-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 1
Pred. No. 0.1;
0; Mismatches
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APPLICATION UNBER: DE P 42 33 646.5
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.6%; SCO
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-471-770-25
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
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Best Local Similarity 100.
Matches 19; Conservative
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                  GERERAL INFORMATION:

APPLICANT: ISALI, Jennifer K.

APPLICANT: Ghosh, Souniter

APPLICANT: Ghosh, Souniter

TITLE OF INVENTION: NON-ISOTOPIC DETECTION OF NUCLEIC ACIDS

TITLE OF INVENTION: USING A POLYSTYRENE SUPPORT-BASED SANDWICH HYBRIDIZATION

TITLE OF INVENTION: ASSAY AND COMPOSITIONS USEFUL THEREFOR

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK

STREET: 444 So. Flower Street, Suite 2000

CITY: LOS Angeles

STARE: CA

CONMINY: USA

ZIP: 90071
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Patent No. 5474895
GENERAL INFORMATION:
APPLICANT: Ishii, Jennifer K.
APPLICANT: Ghosh, Soumitra
TITLE OF INVENTION: USING A POLYSTYRENE SUPPORT-BASED SANDWICH HYBRIDIZATION
TITLE OF INVENTION: ASSAY AND COMPOSITIONS USEFUL THEREFOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 So. Flower Street, Suite 2000
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LOCATION: 1..30
OTHER INFORMATION: /note- "86-272 OLIGONUCLEOTIDE"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPLICATION NUMBER: US/08/050,441
FILING DATE: 05-MAY-1993
CLASSIPRCATION: 435
FILING APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/613,174
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie S.
REGISTRATION NUMBER: 33,779
REPERBUNC/POCKET NUMBER: P51 9633
TELECHONE: 619-546-4737
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: NUCleic acid
STRANDENES: single
                      Sequence 1, Application US/08050441
Patent No. 5474895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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hes 17; Conservative
US-08-050-441-1/c
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US-08-050-441-3
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COUNTRY: LOS Angeles

STATE: CA CAURTRY: USA

ZIP- 30071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IN PC Compatible
COMPUTER: IN PC COMPUTES:

COMPUTES: IN COMPUTES:

COMPUTER: IN COMPUTES:

COMPUTER: IN COMPUTES:

COMPUTER: IN COMPUTES:

CLASSIFICATION NUMBER: US/08/050,441

FELING DATE: 13 779

REPERENCE, CONCET NUMBER: P51 9633

FELING DATE: 10 NO: 3:

COMPUTES: SIGNATION:

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                2054640 seqs, 14551402878 residues
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                                OM nucleic - nucleic search, using sw model
                                                                                                    1 AATGGCAGTCTAGCAGAAGA
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 50
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Perfect :
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Pred. No. is the number of results predicted by chance to have a

PAT 08-JUL-1996

linear

DNA

ALIGNMENTS

Synthetic HIV-1/2 diagnosis primer. A31977

A31977.1 GI:1567260

LOCUS DEFINITION ACCESSION VERSION KEYWORDS

RESULT A31977 SOURCE ORGANISM

REFERENCE AUTHORS TITLE

synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 23)
Moncany,M. and Montagnier,L.
Moulectide sequences of retroviral genomes of types HIV-1, HIV-2
and SIV, their uses for the amplification of these genomes and
diagnosis in vitro of these viral infections

116038 Sequence 1 116640 Sequence 3 116841 Sequence 3 136475 Sequence 2 136475 Sequence 2 136474 Method for AR10575 Sequence E63444 Method for AR068041 Sequence 143893 Sequence 2 A4487597 Caenorhab AR159841 Sequence A63249 Sequence 18 E31336 Process for A63250 Sequence 19 E31377 Process for 128571 Sequence 24 AR08716 Sequence 24 AR150615 Sequence AR200489 Sequence E3606 Higher-orde I42186 Sequence I4228 Sequence 21 I49624 Sequence 39 AR045799 Sequence AR045803 Sequence AR131396 Sequence BD001801 Immunogen AR01371 Sequence AR01301 Sequence AR170661 Sequence AX210201 Sequence AX210201 Sequence AR08233 Sequence AR120881 Sequence AR120881 Sequence A31977 Synthetic H Sequence 25 AR059442 Sequence AX001375 Sequence BD000304 CDNA_comp Sequence 18 Method for Method for score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. A38018 SUMMARIES I63575 AR105726 CEL487597 AR079771 AR081301 AR170661 AX210201 A46935 AR082339 AR120881 AR207576 I78385 E37099 E63428 A38018 AR059442 AR159841 A63249 E31336 A63250 E31337 AR087169 AR150615 AR200489 BD000304 DB Length Query 100.0 100.0 100.0 100.0 100.0 Score υo 000000000

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/organism-"unknown"
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AR081301
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Moncany,M. and Montagnier,L.
Moncany,M. and Montagnier,L.
Nucleotide sequences derived from the genome of retroviruses of the HIV-1, HIV-2, and SIV type, and their uses in particular for the amplification of the genomes of these retroviruses and for the vitro diagnosis of the diseases due to these viruses
Patent: US 6194142-A 48 27-FEB-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 31-JAN-2002
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             LA RECHERCHE
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Patent: JP 2000093187-A 48 04-APR-2000;
Patent: JP 2000093187-A 48 04-APR-2000;
ON TATENT NATL DE LA SANTE 6 DE LA RECHERCHE MEDICAL OS Artificial Sequence
PN JP 2000093187-A/48
PD 04-APR-2000
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Patent: EP 0403333-A 32 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE
MEDICALE (INSERM)
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Pred. No. 0.13;
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/db_xref="taxon:32630" 3 t
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Sequence 48 from patent US 6194142.
AR131396.1 GI:14120299
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1 (bases 1 to 23)

Moncany, M. and Montagnier, L.
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                                           Location/Qualifiers
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BD001801.1 GI:18626360
JP 2000093187-A/48.
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Best Local Similarity 100.0%;
Matches 23; Conservative 0
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Best Local Similarity 100.
Matches 23; Conservative
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BD001801
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PR 24-SEP-1999 JP 1999270165
PR 02-JUN-1989 FR 89/07354,20-SEP-1989 FR 89/12371 PI
MAURICE MONCANY, LUC MONTAGNIER
PC C12M15/09, A61K39/21, A61K48/00, A61P31/18, C07H21/04, C07K14/155,
PC C07K14/16,
PC C12Q1/68,C12Q1/70,G01N33/569,C12N15/00
CC L12Q1/68,C12Q1/70,G01N33/569,C12N15/00
FT SOUTCE Location/Qualifiers
FT SOUTCE /organism='Artificial Secuence'
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Pavlakis, G.N. and Felber, B.K.
Method of eliminating inhibitory/ instability regions of mRNA
Patent: US 5965756.A 95 12-OCT-1999;
Location/Qualifiers
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Pavlakis,G.N. and Felber,B.K.
Nucleic acid constructs containing HIV genes with mutated inhibitory/instability regions and methods of using same patent: uS 597256-A 95 26-OCT-1999;
Location/Qualifiers
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Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
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Sequence 95 from patent US 5972596.
AR081301
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Sequence 95 from patent US 5965726.
AR079771
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Pred. No. (
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PAT 07-MAR-1997

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1 (bases 1 to 20)
Fouchier, R.A. and Schuitemaker, J.
NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTIUM
INDUCING AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN
IMMUNODEFICIENCY VIRUS
PATENT: WO 9528800-0 19 26-0CT-1995;
STICHTING CENTRAAL LAB (NL)
Other publication AU 2150095 951110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.
1 (bases 1 to 20)
Draper.K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
Thympson,J.D.
Partent: US 5972704-A 183 26-OCT-1999;
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Pred. No. 4.9;
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100.0%; Pred. No. 4.9
ive 0; Mismatches
                                              20 bp
Sequence 19 from Patent W09528500.
A46935.
A46935.1 GI:2300955
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/db_xref="taxon:32644"
3 c 7 g
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AR082339
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Unclassified.
1 (bases it o 42)
1 (bases it o 42)
Pavlakis,G.N. and Felber,B.K.
Method of eliminating inhibitory/instability regions of mRNA
Method vof eliminating inhibitors/instability regions of mRNA
Patent: US 6291664.A. 95 18-EEP-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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1 (bases 1 to 22)
Witvrouw,M., Fikkert,V., Pannecouque,C., Cherepanov,P., van
Laethem,K., de Clercq,E., Vandamme,A.M. and Debyser,Z.

    .22
/organism="Human immunodeficiency virus type 1"
/db_xref="taxon:11676"

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7 c 3 g 9 t
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Pred. No. 0.11;
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Patent: WO 015745-A 8 09-AUG-2001;
K.U.Leuven Research & Development (BE)
Location/Qualifiers
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Method for quantitating HIV-provirus DNA linear PAT 31-JAN-2002 E37099 E37099.1 GI:18624781 JP 2000157299-A/3.
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S 2018633687

S 20201057891-A/4.

Synthetic construct.

Synthetic construct.

ISM artificial sequences.

CE 1 (bases 1 to 20.0) 2. Hiraishi,Y., Shimizu,K. and Sugita,T.

Method for determining subtype of HIV-1.

AL Patent: JP 2001057891-A/4

SARC, S. Kobayashi,Y., Shimizu,K. and Sugita,T.

AL Patent: JP 2001057891-A 4 06-WAR-2001;

KETO UNIV

OS Artificial Sequence

PN JP 2001057891-A/4
                                                                                                                                                                                                                                                        artificial sequences.

1 (bases 1 to 20)
Kato,S., Haraishi,Y. and Sugita,T.
Method for quantitating HIV-provirus DNA and diagnosis kit patent: JP 2000157299-A 3 13-JUN-2000;
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Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
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100.0%; Pred. No. 16;
Live 0; Mismatches
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Pred. No.
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JP 2000157299-A/3
13-JUN-2000
30-NOV-1998 JP 1998340303
                        87.0%; Scc.
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Couchier, R. Adrianus. and Schuitemaker, J.

Nucleic acids and methods for the discrimination between syncytium inducing and non syncytium inducing variants of the human immunodeficiency virus

Patent: US 6379881-A 19 30-APR-2002;

Location/Qualifiers
                       Unchassified.

1 (bases 1 to 20)

Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Thompson, J.D.

Method and reagent for inhibiting human immunodeficiency virus replication

Patent: US 6159692-A 183 12-DEC-2000;

Location/Qualifiers
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Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
HIV targeted ribozymes
Patent: US 5693535-A 183 02-DEC-1997;
Location/Qualifiers
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Sequence 183 from patent US 5693535.
178385
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100.0%; Pre
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S Guertler, L.G., Eberle, J.D., Brunn, V.A., Dr, Knapp, S.D. and Hauser, H.D.
Retrovirus of the HIV-group and its application
L Patent: EP 0591914-A 25 13-APR-1994;
BEHRINGWERKE AG (DE)
Other publication AU 4880093 940421
Other publication AP 2107732 940407
Other publication DF 4225760 940816
Other publication DE 4235718 94029
Other publication DE 4235746 940707
Other publication DE 4235766 940816
Other publication DE 4235766 940807
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/organism='Artificial Sequence'
Location/Qualifiers
1.20
/organism="synthetic construct"
/db_xref="taxon:32630" 3 t
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82.6%; Score 19; DB 6; Length 20;
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/organism="unidentified"
/db_xref="taxon:32644"
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Sequence 25 from Patent EP0591914.
A38018
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06-MAR-2001
01-FEB-2000 JP 2000023581
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New nucleotide sequences derived from genome of HIV-1 HIV-2 and SIV - useful as primers for amplification of immuno-deficiency viruses in diagnosis and for raising antibodies in treatment of HIV infections
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AAT62131
AAV09925
AAV09927
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AAF38128
ABL50108
AAQ81322
AAX06932
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AAZ61215
AAZ56626
ABL50154
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  WPI; 1990-378039/51.
HIV-1; AIDS;
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HIV-1 subtype dete
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                                                                                 (without alignments)
251.936 Million cell updates/sec
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1. /SIDS2/gcgdata/geneseg/genesegn-embl/NA1981.DAT:*

2. /SIDS2/gcgdata/geneseg/genesegn-embl/NA1981.DAT:*

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28. /SIDS2/gcgdata/geneseg/genesegn-embl/NA1991.DAT:*

28. /SIDS2/gcgdata/geneseg/genesegn-embl/NA2001.DAT:*

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                                                                                                                                                                                                                              2166140
         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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The present invention describes human immunodeficiency virus type 1 (HIV-1) infectious clones, designated HIV-1-JC and HIV-1-NC. HIV-1-JC and HIV-1-NC are useful for the preparation of recombinant, attenuated and subunit vaccines, as well as for the preparation of challenge stocks. They are also useful in screening for the presence of HIV in biological samples. They can be used for inducing AIDS in a nonhuman primate for the development of a drug or vaccine for the treatment or prevention of AIDS. The present sequence represents a PCR primer used in amplifying the HIV-1-JC env gene.
                                                                                                                                                                                                                                                                                                                  s type 1; HIV-1; infection; AIDS; vaccine; deficiency syndrome; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                       AAX03995;
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                                                                                                                               RESULT 3
AAX03995/c
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AAD13813/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer; PCR; amplification; gag; vpr; pol; vpu; HIV-1; HIV-2; SIV; nef2; v1f2; vpx; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The oligonucleotides AAT98010-T98059 are useful as primers for nucleic
                                                                                                                                                                                                                                                                                   Gaps
                                                      This nucleotide sequence is found in posn. 7055-7077 of HIV-1 Bru, 7053-7075 of HIV-1 Bru, 1055-7077 of HIV-1 Bru, 7053-7075 of HIV-1 Bri. It is the sense strand of a primer pair used to amplify these HIV-1 viral sequences, esp. in conjunction with in vitro diagnosis of infection. This sequence can be expressed in host cells to produce a translation produce useful, in an immunogen, along with Abs raised against it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligo-nucleotide primers for amplifying retroviral nucleic acids - comprising conserved sequences of human immunodeficiency virus and simian immunodeficiency virus genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human or simian immunodeficiency virus detection primer MMy6.
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Pred. No. 0.0052;
                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                              100.0%; Score 23; DB 11; 100.0%; Pred. No. 0.0052;
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                                                                                                                                                                                                         Sequence 23 BP; 10 A; 3 C; 7 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 8; 23pp; French.
                                                                                                                                                                                                                                                                                                                                         1 AATGGCAGTCTAGCAGAAGA 23
                                                                                                                                                                                                                                                                                                                   1 AATGGCAGTCTAGCAGAAGA 23
                       Claim 8; page 21; 24pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus.
Simian immunodeficiency virus.
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100.0%;
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89FR-0007354
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                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 23; Conservative
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02-JUN-1989;
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09-AUG-2001

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woman from Zaire; her serum reacted only moderately with peptides specific for HIV-1, including subgroup O, and reacted with only one African-type V3 peptide. DNA fragments coding for the V3 loop of gpp120 and gp41 from strain MAD were sequenced and analysed. Peptides derived from V3 loops of the new HIV-1 strain are useful in vaccines and for immunodiagnosis. The present sequence represents a claimed oligonuclectide primer for amplifying DNA coding for the V3 loop of HIV-1 strain MAD envelope glycoprotein gp120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new strain of HIV-1 was isolated from a seropositive, asymptomatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus; HIV-1; envelope glycoprotein gp120; variable loop; Zaire; acquired immune deficiency syndrome; AIDS; vaccine; immunodiagnosis; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                              New HIV-1 strain MAD and related nucleic acids and peptide(s) useful for diagnosing HIV-1 infections and generating vaccines
                                                                                                                                                                                                                                                         Chamaret S, Cohen J, Guetard D, Montagnier L, Philbert F;
Tabary T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guetard D, Montagnier L, Philbert F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 91.3%; Score 21; DB 17; Length 21; Best Local Similarity 100.0%; Pred. No. 0.058; Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                       (INSP ) INST PASTEUR
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                                                                                                                                09-FEB-1995;
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                                             FR2730493-A1
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                                                                                         14-AUG-1996.
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    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to recombination assay for the HIV

(Human immunodeficiency virus) envelope genes, gp120, gp41 and gp160.

(Human immunodeficiency virus) envelope genes, gp120, gp41 and gp160.

(Coptimisation of the PCR amplification of the corresponding env-genes and the subsequent sequencing of these genes. These techniques have been applied on several HIV-1(NL4.3) strains selected in vitro in the presence of increasing concentrations of inhibitors of HIV entry and evaluated for the phenotypic resistance of these recombined viruses. This phenotypic resistance has been correlated with genotypic resistance has been correlated with genotypic resistance. The invention also involves a recombination assay for the integrase gene. Determining susceptibility of HIV is useful to study molecular target and resistance profile of action of compounds with anti-HIV activity and to adapt chemotherapy administered to an HIV patient. A genetic information data set on anti-HIV resistance is a useful to influence anti-HIV therapy. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                        Pannecouque C, Cherepanov P, Van Laethem K;
, Debyser 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining susceptibility of HIV isolate to anti-HIV compounds, by excising sequence encoding viral glycoprotein, processing, co-transfecting and culturing cell with obtained isolates, harvesting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                         Recombination assay; HIV; Human immunodeficiency virus; integrase; phenotypic resistance; genotypic resistance; molecular target study; chemotherapy; envelope gene; gpl20; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus; HIV-1; envelope glycoprotein gp120; variable loop; Zaire; acquired immune deficiency syndrome; AIDS; vaccine; immunodiagnosis; polymerase chain reaction; PCR; ss.
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gp120 gene sequencing primer, AV307.
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                                                                                                                                                                                                                                                                05-FEB-2001; 2001WO-BE00017
                                                                                                                                                                                                                                                                                                         04-FEB-2000; 2000GB-0002533.
15-JAN-2001; 2001GB-0001011.
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De Clercg E, Vandamme A,
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Matches 22; Conservative
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AAT42143;

RESULT 5 AAT42143

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evaluation of the efficacy of anti-HIV-1 treatment. Sequences AAA72017-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method and diagnostic kit for the quantitative analysis of HIV-1 provirus DNA, and to a marker for the effective treatment of anti-HIV-1 therapy. The method and kit of the invention can be used for the evaluation of progress of HIV-1 related diseases and/or efficacy of anti-HIV-1 therapy. The invention discloses comprising annealing a primer which is partially complementary to HIV-1 provirus DNA and performing an amplification reaction in which the reaction mixture is incubated at 48+/-4 degrees Celsius and then 64+/-4 degrees Celsius at least once for each step. This is performed in the presence of a known amount of competitor DNA, and the amplified HIV-1 proviral DNA is isolated and quantified. The invention provide effective means for the diagnosis and staging of HIV-1 infection, and for the
                                                                                                                                                                                                                                                                                        Gaps
                                                                                           woman from Zaire; her serum reacted only moderately with peptides specific for HIV-1, including subgroup 0, and reacted with only one African-type V3 peptide. Peptides derived from V3 loops of the new HIV-1 strain are useful in vaccines and for immunodiagnosis. The present sequence repersents an oligonucleotide primar which was used for amplifying DNA coding for the V3 loop of HIV-1 envelope glycoprotein gp120 from various viral strains. A comparison of
                                                                                asymptomatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proviral DNA; quantitative analysis; competitive nested PCR;
                                                                                                                                                                                          different strains allowed the immunodominant epitope of HIV-1 MAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A method and a diagnosis kit for quantitative analysis of HIV-1 provirus \operatorname{DNA} -
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            /-1 strain MAD and related nucleic acids and peptide(s) for diagnosing HIV-1 infections and generating vaccines
                                                                                                                                                                                                                                                         91.3%; Score 21; DB 17; Length 33; 100.0%; Pred. No. 0.058; 1ve 0; Mismatches 0; Indels
                                                                              strain of HIV-1 was isolated from a seropositive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-1 proviral DNA inner PCR primer, SEQ ID NO:3.
                                                                                                                                                                                                                                 Seguence 33 BP; 11 A; 7 C; 11 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic marker; inner PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 4; 11pp; Japanese.
            New HIV-1 strain MAD and related
                                                 Example; Page 12; 24pp; French
                                                                                                                                                                                                                                                                                                                                                                                                               ВЪ.
                                                                                                                                                                                                                                                                                                                 1 AATGGCAGTCTAGCAGAAGAA 21
                                                                                                                                                                                                                                                                                                                                13 AATGGCAGTCTAGCAGAAGAA 33
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                                                                                                                                                                                                                                                                                     21; Conservative
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                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                        to be identified.
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                                                                                                                                                                                                                                                            Query Match
                          useful
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                                                                                A new
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for determining the subtype of human immunodeficiency virus (HIV-1). The method comprises: (a) nucleic acid amplification of the 5' terminal and/or 3' terminal of the nucleotide sequence of the HIV-1 env (envelope) gene, which differs according to the sub-type, as a target sequence; and (b) detecting whether or not the target sequence is present. The method is used to determine a subtype of human immunodeficiency virus (HIV-1). AAF26899 to AAF26842 represent PCR primers used in the exemplification of the method.
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1; subtype; human immunodeficiency virus; detection; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining the subtype of human immunodeficiency virus (HIV)-1, comprises nucleic acid amplification of the termini of the HIV-1
AAA72027 represent HIV-1 PCR primers used in the method of the invention. Sequences AAA72019-A72020 are outer primers used in competitive nested PCR in an exemplification of the invention.
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0
                                                                                                                                                       82.6%; Score 19; DB 21; Length 20; 100.0%; Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                Indels
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1 subtype determining PCR primer SEQ ID NO:4.
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0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hiraishi Y, Shimizu K,
                                                                                                      Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                       Pred. No. 0.6
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characterisation; env; envelope; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 33; 63pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2000; 2000JP-0023581.
                                                                                                                                                                                                                                                                                              2 AATGGCAGTCTAGCAGAAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2000; 2000WO-JP03896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAKA ) OTSUKA PHARM CO LTD.
                                                                                                                                                                                                                                                              1 AATGGCAGTCTAGCAGAAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0167736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF26812 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 100.
Matches 19, Conservative
                                                                                                                                                                                  Local Similarity 100.
Les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kato S, Kobayashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-168279/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYKE-) UNIV KEIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (envelope) gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2001
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                                                                                                                                                          Query Match
                                                                                                                                                                                       Best Loca
Matches
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11-JUN-2002

ABL50092;

RESULT 9 ABL50092

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HIV-type retrovirus; MVP-5180/91; ECACC V 92092318; antigen; assay klt; detection; antibody; immune deficiency; vaccine; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes the isolation of a novel HIV-type retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New HIV-type retrovirus and corresponding cDNA, recombinant DNA and antigen - used for detecting retro-viruses that cause immune deficiency and to prepare vaccines
                                                                                                                                                                                                                  New HIV-type immune deficiency virus ECACC V 92092318 - and deriv. cDNA or antigens, useful for diagnosing retroviral infections and vaccines
                                                                                                                                                                                                                                                                                                                        MVP-5180/91 DNA is obtained by PCR using the primers given
                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 15; Length 31;
Pred. No. 0.63;
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                                                                                                                                                     Hauser H-P,
                                                                                                                                                                                                                                                                                                                                                                         Sequence 31 BP; 10 A; 6 C; 10 G; 5 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guertler LG,
                                                                                                                                                     Gurtler LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BEHRING MARBURG GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 4; 39pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                         82.6%; Sconstity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                               92DE-4233646.
92DE-4235718.
92DE-4244541.
93DE-4318186.
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92DE-4233646.
92DE-4235718.
93EP-0116058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 GGCAGTCTAGCAGAAG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93EP-0116058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92DE-4244541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GGCAGTCTAGCAGAAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX22350 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                        Disclosure; Page 5; 73pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV-1 PCR primer 5v3deg1.
                                                                                                                   (BEHW ) BEHRINGWERKE AG
                                                                                                                                                     Eberle J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brunn AV, Eberle J,
                                                                                                                                                                                    WPI; 1994-120077/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-072878/07
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                         in AAQ58925-958
                               06-0CT-1992;
22-0CT-1992;
30-DEC-1992;
01-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DADE-) DADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1993;
06-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-0CT-1993;
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30-DEC-1992;
05-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-1999
                                                                                                                                                   Brunn VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX22350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for detecting HIV-1. The method comprises an amplification reaction using part of the nucleotide sequence of the HIV-1 env gene as the target sequence and confirming the presence or the absence of HIV-1 by the presence this sequence. The sequence is highly conserved between a number of subtypes. The present 'Invention also describes: (1) a primer which is part of the nucleotide sequence of env gene of HIV-1; and (2) a kit for detecting HIV-1 comprising a primer pair. The present sequence represents a PCR primer for the HIV-1 env gene which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                      SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus; HIV; antigen; detection; diagnosis;
retrovirus; vaccine; lymphocyte; reverse transcriptase;
amplification; primer; polymerase chain reaction; PCR; ss.
                                                                                                                                                                   virus; HIV-1; detection; env; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of HIV-1 comprises amplification using the nucleotide sequence of the env gene of {\rm HIV}{\rm -1} as the target -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 0.63;
0; Mismatches 0; Indels
                                                                                                                                 HIV-1 env gene detection PCR primer 10 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                    Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 5; 20pp; Japanese
                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     вР
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larity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AATGGCAGTCTAGCAGAAG 20
                                                                                                                                                                                                                                                                                                      28-JUN-2000; 2000JP-0194968
                                                                                                                                                                                                                                                                                                                                        28-JUN-2000; 2000JP-0194968
                               ABL50092 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                         (KEIO-) GH KEIO GIJUKU.
                                                                                                                                                                 Human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention.
                                                                                                                                                                                                                                    JP200200277-A.
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04 - NOV - 1994

AAQ58949;

RESULT 10

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AAQ58949

Query Match

Best Loca Matches

13-APR-1994 EP591914-A

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Gaps

888888888

RESULT 12

ð g AAN80773

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Probe for HIV-1 virus. It can be derivatized at the 5'- and 3'-terminal.
                                                                                       Lanthanide chelate-tagged probe; HIV-1 virus; human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer used to target HIV-1 virus allows for it's rapid duplication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymerase extension; gene amplification; PCR; HIV-1; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                        Lanthanide chelate-tagged nucleic acid probes
- used in hybridisation assays with high sensitivity
due to intense fluorescence of the ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription-based nucleic acid amplification -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.9%; Score 17; DB 10; Best Local Similarity 100.0%; Pred. No. 7; Matches 17; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30 BP; 6 A; 9 C; 2 G; 13 T; 0 other;
                                                                                                                                     Human immunodeficiency virus 1 (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example II (B); page 61; 94pp; English
                                                                                                                                                                                                                                                                                                                                TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kwoh DY;
                                                                                                                                                                                                                                                                                                                              Gingeras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                               (SISK-) SISKA DIAGNOSTICS I.
                                                                                                                                                                                                                                 88WO-US03735
                                                                                                                                                                                                                                                                87US-0112855
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88US-0202978
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AAN94510/c
ID AAN94510 standard; DNA; 30
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SISK ) SISKA DIAGNOST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merten U,
                                                       Probe for HIV-1 virus.
                                                                                                                                                                                                                                                                                                                             Musso GF, Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-165653/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1989-023856/03
                                                                                                                                                                                                                                 21-OCT-1988;
                                                                                                                                                                                                                                                                23-OCT-1987;
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                        14-FEB-1990
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06-JUN-1988;
                                                                                                                                                                  WO8904375-A.
                                                                                                                                                                                                   18-MAY-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAN94510;
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                                                                                                                                                                                                 ö
called MVP-5180/91 (ECACC V 92092318). Antigens produced from this product can be used in an assay kit for detecting antibodies against viruses that cause immune deficiency, preferably where the assay is a Western blot, ELISA or fluorescence immunoassay. MVP-5180/91, cDNA and/or antigen can be used for detecting retroviruses that cause immune deficiency and to prepare vaccines. This sequence represents a PCR primer used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuc. acid probe assay – using a probe which is end-attached to a support and a labelled probe with a sequence non complementary to the 1st probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This probe can alternatively be RNA and is used in an assay for HIV-1. (Updated on 03-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                 Gaps
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                                                                                                                                                               Score 19; DB 20; Length 31;
Pred. No. 0.63;
                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 30;
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100.0%; Pred. No. 7;
tive 0; Mismatches (
                                                                                                                                Sequence 31 BP; 10 A; 6 C; 10 G; 5 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30 BP; 6 A; 9 C; 2 G; 13 T; 0 other;
                                                                                                                                                            Query Match
82.6%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 0.6
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN92234 standard; DNA; 30 BP.
                                                                                                                                                                                                                                                                                                                                       AAN80773 standard; DNA; 30 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe for detection of HIV-1.
                                                                                                                                                                                                                            4 GGCAGTCTAGCAGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87WO-US01966.
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                                                                                                                                                                                                                                            13 GGCAGTCTAGCAGAAGAAG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86US-0895756
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(first entry)
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1988-064017/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2002
16-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gingeras TR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO8801302-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1988
                                                                                                                                                                                                                                                                                                                                                                      AAN80773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting single-stranded target nucleic acid - by hybridisation to oligo:nucleotide(s) bonded to polystyrene support and detection with oligo:nucleotide(s)
                                                                                                                                              3'-Primer subsegment 1 in the presence of a polymerase, enables amplification of a sequence within the genome of HIV-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of detection oligonucleotide 86-272 for HIV-1 envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection probe; capture probe; primer; HIV-1 envelope protein; hybridisation; ss.
using nucleic acid primers corresp. to a segment of a target sequence and a polymerase extension.
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                                                                                                                                                                                                                                                                                               Length 30;
                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                         Query Match 73.9%; Score 17; DB 10; Best Local Similarity 100.0%; Pred. No. 7; Matches 17; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                      Sequence 30 BP; 6 A; 9 C; 2 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 30 BP; 6 A; 9 C; 2 G; 13 T; 0 other;
                                                                                        Claim 48; Page 74; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example, Page 24; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SISK-) SISKA DIAGNOSTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0613174.
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ID AAQ25361 standard; DNA; 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sednence.
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